

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 1, 2003, 15:12:47 ; Search time 23 Seconds
(without alignments)
710.508 Million cell updates/sec

Title: US-09-939-484-4

Perfect score: 2042

Sequence: 1 MKRQNVRLALIVCTFTYLL.....STGHSHLSTFRGLMKRRSSV 394

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Swissprot_40;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB ID Description

Result No.	Score	Match	Length	DB	ID	Description
1	2042	100.0	394	1	CIW3_HUMAN	014649 homo sapien
2	1850.5	90.6	411	1	CIW3_MOUSE	054912 rattus norvegicus
3	1840.5	90.1	409	1	CIW3_RAT	035111 mus musculus
4	1116	54.7	374	1	CIW9_HUMAN	039158 cavia porcellus
5	1065.5	52.4	365	1	CIW9_MOUSE	P97438 mus musculus
6	370	18.1	411	1	CIW2_MOUSE	P05069 homo sapiens
7	364	17.8	426	1	CIW4_HUMAN	P57789 homo sapiens
8	348.5	17.1	538	1	CIW4_RAT	Q9J154 rattus norvegicus
9	349.5	17.1	538	1	CIW4_MOUSE	Q9YQ98 homo sapiens
10	328.5	16.1	393	1	CIW4_HUMAN	Q88454 mus musculus
11	326.5	16.0	398	1	CIW4_MOUSE	Q00188 homo sapiens
12	320.5	15.7	336	1	CIW4_HUMAN	Q05279 homo sapiens
13	319	15.6	499	1	CIW4_MOUSE	Q08581 mus musculus
14	318	15.6	336	1	CIW1_MOUSE	Q9Y257 homo sapiens
15	295.5	14.5	313	1	CIW6_HUMAN	Q94526 drosophila melanogaster
16	267.5	12.8	1001	1	ORKL_DRONE	P34410 caenorhabditis elegans
17	259.5	12.8	335	1	TWKB_CAEEL	Q9Y262 homo sapiens
18	224	11.0	307	1	CIW7_HUMAN	Q9Y261 mus musculus
19	221	10.8	307	1	CIW7_MOUSE	P02271 mus musculus
20	170	8.3	691	1	TKYL YEAST	P04310 saccharomyces cerevisiae
21	112.5	5.5	490	1	CIKL_DRONE	P17971 drosophila melanogaster
22	100	4.9	694	1	FZDR_HUMAN	Q9h461 drosophila melanogaster
23	99.5	4.9	174	1	CIKE_DRONE	P02280 drosophila melanogaster
24	98	4.8	1743	1	TAGC_DICOT	P02386 drosophila melanogaster
25	97.5	4.8	228	1	YWSL_CAEEL	Q10937 caenorhabditis elegans
26	97.5	4.8	432	1	A2AR_LABOS	P19182 labiosus
27	96.5	4.7	449	1	IRFL_MOUSE	mus musculus
28	94.5	4.6	209	1	1139_MEUTA	Q57603 methanococcus maripalae
29	94.5	4.6	385	1	PER_DRONE	P91686 drosophila melanogaster
30	94.5	4.6	449	1	IFRL1_RAT	P20695 rattus norvegicus
31	94.5	4.6	647	1	KNRL1_DRONE	P13054 drosophila melanogaster
32	94	4.6	262	1	VG38_BPT2	P07875 bacteriophaga
33	94	4.6	287	1	WC2A_ARATH	P43286 arabidopsis thaliana

ALIGNMENTS

34	94	4.6	1159	1	HERG_HUMAN	Q12809 homo sapiens
35	93.5	4.6	285	1	WC2C_ARATH	P30302 arabidopsis thaliana
36	93	4.6	529	1	CIK6_HUMAN	P17658 homo sapiens
37	93	4.6	602	1	CIK5_RAT	P1924 rattus norvegicus
38	92.5	4.5	565	1	DSBD_ECO57	P58162 escherichia coli
39	92.5	4.5	653	1	CIK4_HUMAN	P22459 homo sapiens
40	92.5	4.5	655	1	CIK4_RAT	P15385 rattus norvegicus
41	92.5	4.5	685	1	FZDB_MOUSE	P061091 mus musculus
42	92	4.5	451	1	IRFL1_HUMAN	P00458 homo sapiens
43	92	4.5	598	1	CIK5_RABBIT	P50638 oryctolagus cuniculus
44	91.5	4.5	660	1	CIK4_BOVIN	P05037 bos taurus
45	91.5	4.5	1581	1	VGLP_BEV	P23052 bovine virus

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CC	entities requires a license agreement. (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
DR	EMBL: AF006923; AAC5177.1; -
DR	EMBL: AF065163; AAG2940.1; -
DR	Genew: 62278; KCNK3.
DR	MIM: 603220; IPR03280; K+channel_2pore.
DR	InterPro: IPR01622; K+channel_pore.
DR	InterPro: IPR00636; M+channel_pdg.
DR	InterPro: IPR03092; TASK_Channel.
DR	PFam: PF00220; Ion_trans; 1.
DR	PRINTS: PRO1333; 2POREKCHANNEL.
DR	PRINTS: PRO1095; TASKCHANNEL.
KW	Ionic channel; Transmembrane; Ion transport; Potassium transport;
FT	Glycoprotein. 1 8 CYTOPLASMIC (POTENTIAL).
FT	DOMAIN 9 29 POTENTIAL.
FT	TRANSMEM 78 101 PORE-FORMING 1 (POTENTIAL).
FT	TRANSMEM 108 128 POTENTIAL.
FT	DOMAIN 129 158 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 159 179 POTENTIAL.
FT	DOMAIN 184 207 PORE-FORMING 2 (POTENTIAL).
FT	TRANSMEM 223 243 CYTOPLASMIC (POTENTIAL).
FT	DOMAIN 244 394 CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD 53 53 N-LINKED (GLCNAC. -) (POTENTIAL).
SQ	SEQUENCE 394 AA: 43518 MW: 945482666F15FB7 CRC64;
Query Match	100.0%; Score 2042; DB 1; Length 394;
Best Local Similarity	100.0%; Pred. No. 1e-153;
Matches	394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 MKRQNRVTLALIVCTFTYLLVGAVALQDALESEPELIERQRLRQELRARRYNLSQGGE 60
Db	1 MKRQNRVTLALIVCTFTYLLVGAVALQDALESEPELIERQRLRQELRARRYNLSQGGE 60
Qy	61 ELERVVLRKPHKAGVWRFGSEFYFAITVITVIGHAAAPSTDGKVFCKMFALLGPI 120
Db	61 ELERVVLRKPHKAGVWRFGSEFYFAITVITVIGHAAAPSTDGKVFCKMFALLGPI 120
Qy	121 TLVMFQSLGERINTLVLRLRAKKLGMRRADVSMANVLLGFFSCISTLCIGAAFTSH 180
Db	61 ELERVVLRKPHKAGVWRFGSEFYFAITVITVIGHAAAPSTDGKVFCKMFALLGPI 120
Qy	121 TLVMFQSLGERINTLVLRLRAKKLGMRRADVSMANVLLGFFSCISTLCIGAAFTSH 180
Db	121 TLVMFQSLGERINTLVLRLRAKKLGMRRADVSMANVLLGFFSCISTLCIGAAFTSH 180
Qy	181 YEHWTFFQAVYCFITLTIGFGDYVALQDAQLOTOPOVAFSEPVYIITGLTVIGAFLN 240
Db	181 YEHWTFFQAVYCFITLTIGFGDYVALQDAQLOTOPOVAFSEPVYIITGLTVIGAFLN 240
Qy	241 LVLRLFMMNAEDEKDRAEHRLALTQAGGGGGSAHTDTASSTAAAGGGFRWY 300
Db	241 LVLRLFMMNAEDEKDRAEHRLALTQAGGGGGSAHTDTASSTAAAGGGFRWY 300
Qy	301 AEVLHFQSMCSCIWYKREKLOQSIPTMIPDLSSTDTCVEQSHSPGGGRYSDTPRR 360
Db	301 AEVLHFQSMCSCIWYKREKLOQSIPTMIPDLSSTDTCVEQSHSPGGGRYSDTPRR 360
Qy	361 CLCGSAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394
Db	361 CLCGSAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394
RESULT 2	
CIW3_RAT	STANDARD; PRT: 411 AA.
ID	CIW3_RAT
AC	054912;
DT	16-Oct-2001 (Rel. 40, Created)
DT	16-Oct-2001 (Rel. 40, Last sequence update)
DE	Potassium channel subfamily K member 3 (acid-sensitive potassium channel protein TASK) (TWIK-related acid-sensitive K ⁺ channel).
GN	KCNK3 OR TASK
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Mammalia; Eutheria; Rodentia; Sciuromyath; Muridae; Murinae; Rattus; OC NCBI_TaxID=10116;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE="Cerebellum;"
RX	Medline:98099797; Pubmed=9437008;
RA	Taylor D.M., Chavez R.A., Forseyeth J.R., Yost C.S.;
RA	"An open rectifier potassium channel with two pore domains in tandem cloned from rat cerebellum.";
RA	J. Neurosci. 18:8669-8771(1998).
CC	-!- FUNCTION: PDZ-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM CHANNEL PROTEIN, RECTIFICATION DIRECTION RESULTS FROM POTASSIUM ION CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARD WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW.
CC	(BY SIMILARITY).
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC	EXPRESSION IN LUNG AND BRAIN. LOW LEVELS IN LIVER, KIDNEY AND SKELETAL MUSCLE.
CC	-!- MISCELLANEOUS: INHIBITED BY EXTRACELLULAR ACIDIFICATION, ZINC, BUPIVACAINE AND PHENTOIN ACTIVATED BY PROTEIN KINASE A.
CC	-!- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.
CC
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CC	EMBL: AF031384; AAC3952.1; -
DR	InterPro: IPR03280; K+channel_2pore.
DR	InterPro: IPR01622; M+channel_pdg.
DR	InterPro: IPR03092; TASK_Channel.
DR	PFam: PF00220; Ion_trans; 1.
DR	PRINTS: PRO1333; 2POREKCHANNEL.
DR	PRINTS: PRO1095; TASKCHANNEL.
KW	Ionic channel; Transmembrane; Ion transport; Potassium transport;
FT	Glycoprotein. 1 8 CYTOPLASMIC (POTENTIAL).
FT	DOMAIN 9 29 POTENTIAL.
FT	TRANSMEM 78 101 PORE-FORMING 1 (POTENTIAL).
FT	TRANSMEM 108 128 POTENTIAL.
FT	DOMAIN 129 158 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 159 179 POTENTIAL.
FT	DOMAIN 184 207 PORE-FORMING 2 (POTENTIAL).
FT	TRANSMEM 223 243 POTENTIAL.
FT	DOMAIN 244 411 CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD 53 53 N-LINKED (GLCNAC. -) (POTENTIAL).
SQ	SEQUENCE 411 AA: 45276 MW: D27780.6E09EB2F5 CRC64;
Query Match	90.6%; Score 1850.5; DB 1; Length 411;
Best Local Similarity	88.3%; Pred. No. 1.3e-138;
Matches	363; Conservative 8; Mismatches 23; Indels 17; Gaps 2;
Qy	1 MKRQNRVTLALIVCTFTYLLVGAVALQDALESEPELIERQRLRQELRARRYNLSQGGE 60
Db	1 MKRQNRVTLALIVCTFTYLLVGAVALQDALESEPELIERQRLRQELRARRYNLSQGGE 60
Qy	61 ELERVVLRKPHKAGVWRFGSEFYFAITVITVIGHAAAPSTDGKVFCKMFALLGPI 120
Db	61 ELERVVLRKPHKAGVWRFGSEFYFAITVITVIGHAAAPSTDGKVFCKMFALLGPI 120
Qy	121 TLVMFQSLGERINTLVLRLRAKKLGMRRADVSMANVLLGFFSCISTLCIGAAFTSH 180
Db	121 TLVMFQSLGERINTLVLRLRAKKLGMRRADVSMANVLLGFFSCISTLCIGAAFTSH 180
Qy	181 YEHWTFFQAVYCFITLTIGFGDYVALQDAQLOTOPOVAFSEPVYIITGLTVIGAFLN 240

DT 15-JUN-2002 (Rel. 41, last annotation update)
 DE Potassium channel subfamily K member 9 (acid-sensitive potassium channel, protein TASK-3) (TWIK-related acid-sensitive K+ channel 3).
 GN KCNK9 OR TASK3.
 OS Homo sapiens (Human).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OC NCI_TAXID=9006;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20287530; PubMed=10747866;
 RA Rajan S., Wuschmeier E., Liu G.X., Preisig-Mueller R., Daut J., Karschin A., Drest C.; "Task-3, a novel tandem pore domain acid-sensitive K+ channel. An extracellular histidine as pH sensor.", J. Biol. Chem. 275:16650-16657(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=cerebellum;
 RX MEDLINE=20499203; PubMed=11042359;
 RA Chapman C.G., Meadows H.J., Godden R.J., Campbell D.A., Duckworth M., Kelsell R.E., Murdock P.R., Randall A.D., Renille G.I., Gloger I.S.; "Cloning, functional expression of a novel human, cerebellum specific, two pore domain Potassium channel.", Brain Res. Mol. Brain Res. 82:74-83(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Girard C., Lescage F., Tinel N., Lazdunski M.; "Human Task-3, a novel 2P domain potassium channel related to Task.", Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RL [4]
 RP Vega-Saenz de Miera E.C., Lau D.H.P., Zhadina M., Pountney D., Coetze W., Rudy B.; "Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM CHANNEL PROTEIN.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- TISSUE-SPECIFICITY: MAINLY FOUND IN THE CEREBELLUM.
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.

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CC RESULT 5
 CC CIW9_CAVPO
 CC CIW9_CAVPO STANDARD: PRM: 365 AA.
 CC ID OS1158;
 CC DT 16-OCT-2001 (Rel. 40, Created)
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
 CC DE Potassium channel subfamily K member 9 (acid-sensitive potassium channel, protein TASK-3) (TWIK-related acid-sensitive K+ channel 3).
 CC GN KCNK9 OR TASK3.
 CC OS Cavia porcellus (Guinea pig).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystericognathi; Caviidae; Cavia.
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC TISSUE=Brain;
 CC RX MEDLINE=20287530; PubMed=10747866;
 CC RA Rajan S., Wuschmeier E., Liu G.X., Preisig-Mueller R., Daut J., Karschin A., Drest C.; "Task-3, a novel tandem pore domain acid-sensitive K+ channel. An extracellular histidine as pH sensor.", J. Biol. Chem. 275:16650-16657(2000).
 CC -1- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM CHANNEL PROTEIN.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.

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DR	EMBL: AF212827; AACF33706; 1; -	DR	DR
DR	InterPro: IPR003280; K+channel_2pore.	DR	DR
DR	InterPro: IPR01622; K+channel_pore.	RA	RA
DR	InterPro: IPR00636; M+channel_lig.	RA	Lazdunski M.;
DR	InterPro: IPR003092; TASK_channel.	RT	"Cloning functional expression and brain localization of a novel
DR	Pfam: PF00520; Ion_trans; 1.	RT	"unconventional outward rectifier K+ channel.";
DR	PRINTS; PR01333; 2POREKCHANNEL.	RL	EMBO J. 15:6854-6862 (1996).
DR	Ionic channel; transmembrane; Ion transport; Potassium transport;	RN	[2].
DR	Glycoprotein. 1	RP	REVISONS.
KW	CYTOSOLIC (POTENTIAL).	RP	TISSUE:Brain;
FT	TRANSMEM 9 29	RA	Fink M., Duprat F., Lesege F., Reyes R., Romey G., Heurteaux C.,
FT	DOMAIN 78 101	RA	Lazdunski M.;
FT	TRANSMEM 103 128	RA	Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
FT	DOMAIN 129 158.	RA	[3].
FT	TRANSMEM 159 179	RP	ACTIVATION.
FT	DOMAIN 184 207	RX	MEDLINE:99254548; PubMed-10321245;
FT	TRANSMEM 219 239	RA	Patel A. J., Honore E., Lesege F., Fink M., Romey G., Lazdunski M.;
FT	DOMAIN 240 365	RT	"Inhalational anesthetics activate two-pore-domain background K+ channels.";
FT	CARBOHYD 53 53	RT	CC
SEQUENCE	365 AA; 40769 MW; 261D973FF53AF91 CRC64;	RL	Nat. Neurosci. 2:422-426 (1999).
Query Match	52.4%; Score 1069.5; DB 1; Length 365;	CC	-1- FUNCTION: REACTING POTASSIUM CHANNEL.
Best Local Similarity	57.8%; Pred. No. 3. 9e-77;	CC	-1- SUBUNIT: HOMODIMER (POTENTIAL).
Matches	226; Conservative 43; Mismatches 94; Indels 33; Gaps 6;	CC	-1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
QY	1 MKRQNRTLALLVCTTTCYLYGAFTDALESEPELIERERQRLQOELRARRYNLSSGCGYE 60	CC	-1- TISSUE SPECIFICITY: HIGH EXPRESSION IN BRAIN AND LUNG. ALSO
QY	1 MKKQNRTLSLIACTTYLNGAAVDALESDEHMRBEEKLKAEEERIRGKYNISTEDYR 60	CC	DETECTED IN KIDNEY, HEART AND SKELETAL MUSCLE. NOT DETECTED IN
QY	61 ELERVVLRKLPHKAGQWKRAGPSFYVATVITIGGHAATGAASTDGGKVFCHMAYALLGIPL 120	CC	LIVER, IN THE BRAIN, HIGHEST EXPRESSION IN OLFACTORY BULB,
Db	61 QLEVLVLIQSEPHRAGQWKFAGSFVYAVIGIPL 120	CC	HIPPOCAMPUS AND CEREBELLUM.
QY	121 TLVLFQSLGERINTLYRLLHRRAKKGMRRADVISMANMVLIGFFSCISTICLGAFAFS 180	CC	-1- MISCELLANEOUS: INHIBITED BY BARIUM. ACTIVATED BY VOLATILE GENERAL
Db	121 TLVLFQSLGERINTLYRLLHRRAKKGMRRADVISMANMVLIGFFSCISTICLGAFAFS 180	CC	ANESTHETICS SUCH AS CHLOROFORM, DIETHYL ETHER, HALOTHANE AND
QY	181 YEHWTIFQAYYCFTLTTIGRQDYVALQKDOALQIOPQYAFASFWVLTGLVIGAFLN 240	CC	ISOFLURANE.
Db	181 CEEWSPFHAYVYCFTLTTIGRQDYVALQSKALQRKPFVAFSFMLVILGIVAGFLN 240	CC	-1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
QY	241 LVLRLRPTMNADEDEKAHRHLLTRNGQAGGGGSGSAHTDTAATAA--AGGSFRN 298	CC	CHANNELS.
Db	241 LVLRLRPTMNADEDEERGEGEAGALP----GNPSVWTHLSEEARQVQRVYRGEGG-- 291	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
QY	299 VYAEVHFQSMCSLWYKSRKQYLSIPMIPRDLSTSCTCQEVSQHSSPGGGRYSDTPS 358	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
Db	299 VYAEVHFQSMCSLWYKSRKQYLSIPMIPRDLSTSCTCQEVSQHSSPGGGRYSDTPS 358	CC	the European Bioinformatics Institute. There are no restrictions on its
QY	359 RRLCLCSGAPRASISSWSTGLHSLSTRGLMRRSSV 394	CC	use by non-profit institutions as long as its content is in no way
Db	359 RRLCLCSGAPRASISSWSTGLHSLSTRGLMRRSSV 394	CC	modified and this statement is not removed. Usage by and for commercial
QY	332 -TLMKSLFPSPISSVSPGLHSFGDNHRLMLRKSV 365	CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
Db	332 -TLMKSLFPSPISSVSPGLHSFGDNHRLMLRKSV 365	CC	DR
RESULT 6	DR	EMBL: U73488; AAC53005; 2; -	
CIW2_MOUSE	DR	MGD; MGI:1109366; Kcnk2.	
ID_CIW2_MOUSE	DR	InterPro: IPR003280; K+channel_2pore.	
STANDARD	DR	InterPro: IPR01622; K+channel_pore.	
PRT:	DR	InterPro: IPR00636; M+channel_lig.	
411 AA.	DR	InterPro: IPR003976; Trek_channel.	
	DR	Pfam: PF00520; Ion_trans; 1.	
	DR	PRINTS; PR01333; 2POREKCHANNEL.	
	DR	Ionic channel; transmembrane; Ion transport; Potassium transport;	
KW	Glycoprotein.	RA	DR
FT	DOMAIN 1 46	RA	DR
FT	TRANSMEM 47 67	RA	DR
FT	DOMAIN 129 155	RA	DR
FT	TRANSMEM 157 177	RA	DR
FT	DOMAIN 178 207	RA	DR
FT	TRANSMEM 208 228	RA	DR
FT	DOMAIN 238 268	RA	DR
FT	TRANSMEM 273 293	RA	DR
FT	DOMAIN 294 411	RA	DR
FT	DOMAIN 378 411	RA	DR
FT	DOMAIN 354 411	RA	DR
FT	CARBOHYD 95 95	RA	DR
FT	CARBOHYD 119 119	RA	DR
SEQUENCE	411 AA; 45297 MW; 81976DD0103FA05 CRC64;	RA	DR
MUS musculus (Mouse).	Query Match	18.1%; Score 370; DB 1; Length 411;	
OC	Best Local Similarity	28.0%; Pred. No. 5.8e-22;	
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	Matches	109; Conservative 66; Mismatches 126; Indels 88; Gaps 13;	
NCBI_TAXID=10090;			
[1]	SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.		

RESULT	9	RA	Romeo G.	Lazdunski M.	RX
CINA_RAT		ID	CINA_RAT	STANDARD;	PRT;
CC		AC	Q8TIS4;		538 AA.
CC		RT	GL1, and Gq protein-coupled receptors ",		
CC		RL	J. Biol. Chem. 275:28398-28405(2000).		
CC		RT	-1- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL. PRODUCES RAPIDLY ACTIVATING AND NON-INACTIVATING OUTWARD RECTIFIER K(+) CURRENTS.		
CC		CC	ACTIVATED BY ARACHIDONIC ACID AND OTHER NATURALLY OCCURRING UNSATURATED FREE FATTY ACIDS.		
CC		CC	-1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).		
CC		CC	-1- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN PANCREAS AND KIDNEY AND TO A LOWER LEVEL IN BRAIN, TESTIS, COLON, AND SMALL INTESTINE.		
CC		CC	-1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.		
CC		CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
CC		CC	-----		
CC		CC	Rattus norvegicus (Rat), OC		
CC		CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC		
CC		CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus, OC		
CC		CC	NCBI_TAXID=10116; RN [1]		
CC		CC	RP SEQUENCE FROM N.A.		
CC		CC	RX MEDLINE-20298807; PubMed=10747911;		
CC		CC	RA Bang H., Kim Y., Kim D.;		
CC		CC	RT "TREK-2", a new member of the mechanosensitive tandem-pore K+ channel family.",		
CC		CC	RT J. Biol. Chem. 275:17412-17419(2000).		
CC		CC	-1- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL. PRODUCES RAPIDLY ACTIVATING AND NON-INACTIVATING OUTWARD RECTIFIER K(+) CURRENTS.		
CC		CC	ACTIVATING AND NON-INACTIVATING OUTWARD RECTIFIER K(+) CURRENTS.		
CC		CC	UNSATURATED FREE FATTY ACIDS.		
CC		CC	-1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).		
CC		CC	-1- TISSUE SPECIFICITY: EXPRESSED MAINLY IN THE CEREBELLUM, SPLEEN, AND TESTIS.		
CC		CC	-1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.		
CC		CC	This SWISS-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
CC		CC	-----		
CC		CC	DR InterPro; IPR00636; M+channel_nlg.		
CC		CC	PRIMs; PR0520; Ion_trans; 1.		
CC		CC	DR InterPro; IPR0133; 2POREKCHANNEL.		
CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
CC		CC	DR InterPro; IPR003280; K+channel_pore.		
CC		CC	PRIMs; PR0520; Ion_trans; 1.		
CC		CC	DR InterPro; IPR00636; M+channel_nlg.		
CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
CC		CC	DR InterPro; IPR0133; TREKCHANNEL.		
CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
CC		CC	DR InterPro; IPR00636; M+channel_nlg.		
CC		CC	PRIMs; PR0520; Ion_trans; 1.		
CC		CC	DR InterPro; IPR003280; K+channel_pore.		
CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
CC		CC	DR InterPro; IPR00636; M+channel_nlg.		
CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
CC		CC	DR InterPro; IPR003280; K+channel_pore.		
CC		CC	PRIMs; PR0520; Ion_trans; 1.		
CC		CC	DR InterPro; IPR00636; M+channel_nlg.		
CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
CC		CC	DR InterPro; IPR003280; K+channel_pore.		
CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
CC		CC	DR InterPro; IPR00636; M+channel_nlg.		
CC		CC	PRIMs; PR0520; Ion_trans; 1.		
CC		CC	DR InterPro; IPR003280; K+channel_pore.		
CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
CC		CC	DR InterPro; IPR00636; M+channel_nlg.		
CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
CC		CC	DR InterPro; IPR003280; K+channel_pore.		
CC		CC	PRIMs; PR0520; Ion_trans; 1.		
CC		CC	DR InterPro; IPR00636; M+channel_nlg.		
CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
CC		CC	DR InterPro; IPR003280; K+channel_pore.		
CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
CC		CC	DR InterPro; IPR00636; M+channel_nlg.		
CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
CC		CC	DR InterPro; IPR003280; K+channel_pore.		
CC		CC	PRIMs; PR0520; Ion_trans; 1.		
CC		CC	DR InterPro; IPR00636; M+channel_nlg.		
CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
CC		CC	DR InterPro; IPR003280; K+channel_pore.		
CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
CC		CC	DR InterPro; IPR00636; M+channel_nlg.		
CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
CC		CC	DR InterPro; IPR003280; K+channel_pore.		
CC		CC	PRIMs; PR0520; Ion_trans; 1.		
CC		CC	DR InterPro; IPR00636; M+channel_nlg.		
CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
CC		CC	DR InterPro; IPR003280; K+channel_pore.		
CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
CC		CC	DR InterPro; IPR00636; M+channel_nlg.		
CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
CC		CC	DR InterPro; IPR003280; K+channel_pore.		
CC		CC	PRIMs; PR0520; Ion_trans; 1.		
CC		CC	DR InterPro; IPR00636; M+channel_nlg.		
CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
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CC		CC	DR InterPro; IPR00636; M+channel_nlg.		
CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
CC		CC	DR InterPro; IPR003280; K+channel_pore.		
CC		CC	PRIMs; PR0520; Ion_trans; 1.		
CC		CC	DR InterPro; IPR00636; M+channel_nlg.		
CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
CC		CC	DR InterPro; IPR003280; K+channel_pore.		
CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
CC		CC	DR InterPro; IPR00636; M+channel_nlg.		
CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
CC		CC	DR InterPro; IPR003280; K+channel_pore.		
CC		CC	PRIMs; PR0520; Ion_trans; 1.		
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CC		CC	DR InterPro; IPR003280; K+channel_pore.		
CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
CC		CC	DR InterPro; IPR00636; M+channel_nlg.		
CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
CC		CC	DR InterPro; IPR003280; K+channel_pore.		
CC		CC	PRIMs; PR0520; Ion_trans; 1.		
CC		CC	DR InterPro; IPR00636; M+channel_nlg.		
CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
CC		CC	DR InterPro; IPR003280; K+channel_pore.		
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CC		CC	DR InterPro; IPR00636; M+channel_nlg.		
CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
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CC		CC	DR InterPro; IPR00636; M+channel_nlg.		
CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
CC		CC	DR InterPro; IPR003280; K+channel_pore.		
CC		CC	PRIMs; PR0520; Ion_trans; 1.		
CC		CC	DR InterPro; IPR00636; M+channel_nlg.		
CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
CC		CC	DR InterPro; IPR003280; K+channel_pore.		
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CC		CC	DR InterPro; IPR00636; M+channel_nlg.		
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CC		CC	DR InterPro; IPR003280; K+channel_pore.		
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CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
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CC		CC	DR InterPro; IPR00636; M+channel_nlg.		
CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
CC		CC	DR InterPro; IPR003280; K+channel_pore.		
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CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
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CC		CC	DR InterPro; IPR00636; M+channel_nlg.		
CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
CC		CC	DR InterPro; IPR003280; K+channel_pore.		
CC		CC	PRIMs; PR0520; Ion_trans; 1.		
CC		CC	DR InterPro; IPR00636; M+channel_nlg.		
CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
CC		CC	DR InterPro; IPR003280; K+channel_pore.		
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CC		CC	DR InterPro; IPR00636; M+channel_nlg.		
CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
CC		CC	DR InterPro; IPR003280; K+channel_pore.		
CC		CC	PRIMs; PR0520; Ion_trans; 1.		
CC		CC	DR InterPro; IPR00636; M+channel_nlg.		
CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
CC		CC	DR InterPro; IPR003280; K+channel_pore.		
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CC		CC	DR InterPro; IPR00636; M+channel_nlg.		
CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
CC		CC	DR InterPro; IPR003280; K+channel_pore.		
CC		CC	PRIMs; PR0520; Ion_trans; 1.		
CC		CC	DR InterPro; IPR00636; M+channel_nlg.		
CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
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CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
CC		CC	DR InterPro; IPR00636; M+channel_nlg.		
CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
CC		CC	DR InterPro; IPR003280; K+channel_pore.		
CC		CC	PRIMs; PR0520; Ion_trans; 1.		
CC		CC	DR InterPro; IPR00636; M+channel_nlg.		
CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
CC		CC	DR InterPro; IPR003280; K+channel_pore.		
CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
CC		CC	DR InterPro; IPR00636; M+channel_nlg.		
CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
CC		CC	DR InterPro; IPR003280; K+channel_pore.		
CC		CC	PRIMs; PR0520; Ion_trans; 1.		
CC		CC	DR InterPro; IPR00636; M+channel_nlg.		
CC		CC	PRIMs; PR0520; 2POREKCHANNEL.		
CC		CC	DR InterPro; IPR003280; K+channel_pore.		
CC		CC	PRIMs; PR0520; 2PORE		

KW IONIC CHANNEL; TRANSMEMBRANE; ION TRANSPORT; POTASSIUM TRANSPORT;
KW GLYCOPROTEIN.
FT DOMAIN. 1 20 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 21 41 POTENTIAL.
FT DOMAIN 104 130 PORE-FORMING 1 (POTENTIAL).
FT TRANSMEM 133 153 POTENTIAL.
FT DOMAIN 154 177 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 178 198 POTENTIAL.
FT DOMAIN 212 238 PORE-FORMING 2 (POTENTIAL).
FT TRANSMEM 247 267 POTENTIAL.
FT DOMAIN 268 336 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MUTAGEN 161 161 T>A: NO EFFECT ON CHANNEL ACTIVITY.
SO SEQUENCE 336 AA; 38143 MW; 2A41D951323215D CRC64;

Query Match 15.7%; Score 320.5; DB 1; Length 336;
Best Local Similarity 32.4%; Pred. No. 3.5e-18;
Matches 90; **Conservative** 47; **Mismatches** 102; **Indels** 39; **Gaps** 9;

Qy 11 LIVCTFTYLVLGAFFDALESEPELIERQRL-ELRQQLRARYNLNSQGGYEEELRVRL 69
Db 26 LVIGLYLVLYVFGAVVFSSELPYEDLRLRKLRRFLFEEHCLSEQOLPGLRVIE 85

Qy 70 KPHKAGV-----QWREAGSFSYFAITWVITIGYGHAP-STDGGKVFCMFALLGIPIT 121
Db 86 SNTGVSIVLNSNASGNWNMFTSALFASTVLSITGQHPLSDGKAFCCIVSVIGPFT 145

Qy 122 LVMFQSLGRBINTLVRLRHLRAKKGL-----GMRRADVSMANVVLIGFFCISTLG 174

Db 146 LLETTAVVQRIT-----WHVTRRPVLYFHHRGFSKOVWAVHAVLIGFVTSVCFPRIP 199

Qy 175 AAFPSHYE-HWTFQFOAVYYCIFTLTIGFGDWA---LQKDALQTOPQVVAFSFVYL 229
Db 200 AAVFSVLEDWNFLFESYFCFISLSTIGLGDYVPGEGYNQFREL---YKIGITCYLL 254

Qy 230 TG---LTVIGAFLNLVVL--REMTMMAEDEKRAEH 260

Db 255 LGIITAMLYVLETCFELHLKKERKMFVVKDKDQEDQVH 292

RESULT 13

CTW5_HUMAN STANDARD; PRT; 499 AA.

AC Q95279; 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)

DE Potassium channel subfamily K member 5 (acid-sensitive potassium channel protein TWK-2) (TWK-related acid-sensitive K⁺ channel 2).
GN KCNK5 OR TASK2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TAXID=9606;

RN [1] SEQUENCE FROM N.A.

RC TISSUE=Kidney; MEDLINE=9903043; PubMed=9812978; Keyes R., Duprat F., Lesege F., Salinas M., Farman N., Lazdunski M.; Cloning and expression of a novel pH-sensitive two pore domain K⁺ channel from human kidney.; J. Biol. Chem. 273:30863-30869(1998).

CC -I- FUNCTION: PH DEPENDENT, VOLTAGE INSENSITIVE, OUTWARDLY RECTIFYING POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS LOST AT HIGH EXTERNAL K⁺ CONCENTRATIONS.

CC -I- SUBUNIT: HOMODIMER (POTENTIAL).

CC -I- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -I- TISSUE SPECIFICITY: ABUNDANT EXPRESSION IN KIDNEY, ALSO DETECTED IN LIVER, PLACENTA AND SMALL INTESTINE. IN THE KIDNEY, EXPRESSION IS RESTRICTED TO THE DISTAL TUBULES AND COLLECTING DUCTS. NOT EXPRESSED IN PROXIMAL TUBULES OR GLOMERULI.

CC -I- MISCELLANEOUS: INHIBITED BY QUININE, QUININDINE AND EXTERNAL

RESULT 14

CTW1_MOUSE STANDARD; PRT; 336 AA.

AC Q08581; 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)

DE Potassium channel subfamily K member 1 (inward rectifying potassium channel protein TWK-1).
GN KCNK1.

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TAXID=10090;

Search completed: July 1, 2003, 15:16:07
Job time : 25 secs

1. TISSUE SPECIFICITY: WIDESPREAD EXPRESSION, DELICATED IN ALL TISSUES TESTED, EXCEPT FOR SKELETAL MUSCLE. STRONGEST EXPRESSION IN PLACENTA, PANCREAS, HEART, COLON AND SPLEEN. LOWER LEVELS DETECTED IN PERIPHERAL BLOOD, LEUKOCYTES, LUNG, LIVER, KIDNEY AND THYMUS. LOWEST EXPRESSION DETECTED IN BRAIN.

-1- MISCELLANEOUS: INHIBITED BY INTERNAL ACIDIFICATION AND, TO A SMALL

DEGREES, BY ZINC. NOT INHIBITED BY QUININE, QUINIDINE OR BARIUM.
SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.

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EMBL: AFT34149; AAD22980.1; -
EMBL: AFT17708; AAD24000.1; -
EMBL: AFT281302; AAG10506.1; -
EMBL: AFT281303; AAG10507.1; -
EMBL: BC004367; AAH04367.1; -

GeneW, HNC:0281; RENKU; MIM: 603939; InterPro: IPR001622; K+channel_pore.

InterPro; IPR001779; TWIK1_channel; Pfam; PF00520; ion_trans; 1.

ionic channel; Transmembrane; Ion transport; Potassium transport; Glycoprotein; Alternative splicing.

DOMAIN	TRANSMEM	CYTOSOL	POTENTIAL	POLE-POLE
1	4	1	5	90
2	25	2	5	15
3	4	3	1	1

TRANSMEM DOMAIN	121	141	POTENTIAL.
	142	172	CYTOSMERIC (POTENTIAL).

TRANSFORMING 175 193 223 POTENTIAL.
DOMAIN 199 223 256 POTENTIAL.
TRANSMEM 236 256 POTENTIAL.

DOMAIN 257 313 CYTOPLASMIC (POTENTIAL).
CARBOHYD 79 79 N-LINKED (GLCNAC . . .) (POTENTIAL).
C 79 79

VARSPLIC 1 134 MISSING (IN ISOFORM 2).
MUTAGEN 53 53 C->A: NO CHANNEL ACTIVITY.

TY MATCH SEQUENCE 313 AA; 33/4 MW; 13/9382DEB05/5DB CRC64;

Best Local Similarity 31.7%; Pred. NO. 3.1e-16; Matches 90; Conservative 40; Mismatches 95; Indels 59; Gaps 12;

18 YLLVGAEVDALESEPELIERQRQLELRQELRARN-----LSQGGYEEL 63

1/ YLVIGALLVARLEGPEHARLNAEETLAQOLRSPCVAAPALBAFVERVLAG---RLG 73

74 RVLANASGNSANASDPAWDFASALFFASTLITTVGYGTTPLTDAGKAFSIAFALLGVPT 133

121 TLVMFQSLGERINTLVRYLLHRKKGLGM-----RADVSMANVLIGFFCISTLC-- 172

134 TMLLTASAQRLLSLL--LTHVPLSWLSMRWGDPRRA---ACWHLVALLGWWVTCFL 186

187 VPAVIFAHLEEAWSFLLDAFYCCFISLSTLIGSDYVPGEE---APGCPYRALKWVWTWYL 3423

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 1, 2003, 15:13:42 ; Search time 35 Seconds
(without alignments)
2319.502 Million cell updates/sec

Title: US-09-939-484-4

Perfect score: 2042

Sequence: 1 MKRQNVRLALIVCTFTYLL.....STGLHSLSTFRGLMKRRSSV 394

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPREMBL_21:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rabbit:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteria:*

17: sp_archeap:*

Pred. No. 17 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULTS

No.	Score	Query	Match	Length	DB	ID	Description
1	1732	84.8	392	11	Q9ESM5		Q9ESM5 rattus norv
2	1333	65.3	299	11	Q9QX34		Q9QX34 mus musculu
3	1298.5	63.6	301	11	Q9ESM4		Q9ESM4 rattus norv
4	999	48.9	396	11	Q923V6		Q923V6 rattus norv
5	960.5	47.0	395	11	Q9JLD4		Q9JLD4 rattus norv
6	924	45.2	237	11	Q9ES09		Q9ES09 rattus norv
7	916.5	44.9	318	11	Q9RS510		Q9RS510 rattus norv
8	846	41.4	330	4	Q9H427		Q9H427 homo sapien
9	838	41.0	330	4	Q9H427		Q9H427 homo sapien
10	820	40.2	329	5	Q9J185		Q9J185 caenorhabdi
11	777	38.1	340	5	Q9VHE0		Q9VHE0 drosophila
12	742	36.3	398	5	Q9VFS9		Q9VFS9 drosophila
13	732.5	35.9	270	11	Q9JL57		Q9JL57 cavia porce
14	690.5	33.8	271	11	Q920G1		Q920G1 rattus norv
15	599	29.3	364	5	Q97590		Q97590 caenorhabdi
16	405	18.3	340	5	Q8R1PS		Q8R1PS mus musculu

SUMMARIES

Score	Query	Match	Length	DB	ID	Description	
17	369	18.1	405	11	Q9ERS0		Q9ERS0 rattus norv
18	367	18.0	426	11	Q920B6		Q920B6 rattus norv
19	363	17.8	411	4	Q9NRT2		Q9NRT2 homo sapien
20	361	17.7	294	4	Q9HS91		Q9HS91 homo sapien
21	361	17.7	309	4	Q96T55		Q96T55 homo sapien
22	358	17.5	408	4	Q9HB14		Q9HB14 homo sapien
23	357.5	17.5	543	4	Q8TDK8		Q8TDK8 homo sapien
24	349.5	17.1	543	4	Q8TDK7		Q8TDK7 homo sapien
25	349.5	17.1	419	4	Q96194		Q96194 homo sapien
26	329.5	16.1	408	4	Q96E79		Q96E79 homo sapien
27	325	15.9	498	5	Q22940		Q22940 caenorhabdi
28	324	15.9	502	11	Q9JK52		Q9JK52 mus musculu
29	319.5	15.6	336	11	Q9ZT2		Q9ZT2 rattus norv
30	319.5	15.6	336	11	Q99199		Q99199 mus musculu
31	319.5	15.6	397	11	Q92414		Q92414 rattus norv
32	317.5	15.5	336	11	Q8R454		Q8R454 cavia porce
33	310.5	15.5	430	4	Q9HB15		Q9HB15 homo sapien
34	309.5	15.2	430	11	Q9ERS1		Q9ERS1 rattus norv
35	302	14.8	259	6	Q02821		Q02821 orctolagus
36	294.5	14.4	332	4	Q96T54		Q96T54 homo sapien
37	294.5	14.4	332	4	Q8TAW4		Q8TAW4 homo sapien
38	293	14.3	393	5	Q9XU07		Q9XU07 caenorhabdi
39	288	14.1	229	4	Q9HS92		Q9HS92 homo sapien
40	288	14.1	343	4	Q9BXD1		Q9BXD1 homo sapien
41	281.5	13.8	385	5	Q9VYV5		Q9VYV5 drosophila
42	278.5	13.6	592	5	Q9W4G2		Q9W4G2 drosophila
43	278.5	13.6	995	5	Q9W2L7		Q9W2L7 drosophila
44	276.5	13.5	313	11	Q9EUS5		Q9EUS5 rattus norv
45	275	13.5	524	5	Q21729		Q21729 caenorhabdi

ALIGNMENTS

RESULT 1

ID	Q9ESM5	PRELIMINARY	PRT	392 AA.
1	Q9ESM5			
2	Q9ESM5;			
3	DT 01-MAR-2001 (TREMBL; 16, Last sequence update)			
4	DT 01-JUN-2002 (TREMBL; 21, Last annotation update)			
5	DE TASK1 splice bvariant (TAKS1B).			
6	GN KCNKB.			
7	OS Rattus norvegicus (Rat).			
8	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
9	OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus;			
10	OC NCBI-TAXID=10116;			
11	RN [1]			
12	RP SEQUENCE FROM N.A.			
13	RC TISSUE=BRAIN;			
14	RA Ohya S., Kitaoka M., Imaizumi Y.;			
15	RT "TAKS1 splice bvariant (TAKS1B) (KCNKB);			
16	RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.			
17	DR EMBL; AB048823; BAB67101; -			
18	DR InterPro; IPR003280; K+channel_pore.			
19	DR InterPro; IPR001622; K+channel_pore.			
20	DR InterPro; IPR000636; M+channel_lng.			
21	DR InterPro; IPR003092; TASK_channel.			
22	DR Pfam; PF00520; ion_trans; 1.			
23	DR PRINTS; PRO1333; 2POREKCHANNEL.			
24	DR PRINTS; PRO1584; TASKCHANNEL.			
25	DR SEQUENCE; 392 AA; 43150 MW; F5438B12AAD7FB1B CRC64;			
26	DR Query Match 84.8%; Score 1732; DB 11; Length 392; Matches 345; Conservative 83.9%; Pred. No. 1.8e153; Best Local Similarity 83.9%; Pred. No. 1.8e153; Mismatches 23; Indels 36; Gaps 4;			
27	DR QY 1 MKRQNVRLALIVCTFTYLLVGAADFALSEPELTERQELRQBLRQLRNLSSQGYE 60			
28	DR QY 1 MKRQNVRLALIVCTFTYLLVGAADFALSEPELTERQELRQBLRQLRNLSSQGYE 41			

RESULT 2

Q90X34 PRELIMINARY; PRT; 299 AA.

AC Q90X34; DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Putative potassium channel Dp4 (Fragment).
GN KCNK3.
OS Mus musculus (Mouse).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Q90X34
RA Gan L., Joiner W.J., Quinn A.M., Wang L.-Y., Hughes T.,
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP02281; AD0938.1; -.
DR MG1:1100509; Kcnf3.
DR InterPro; IPR00380; K+channel_2pore.
DR InterPro; IPR00622; K+channel_pore.
DR InterPro; IPR00036; M+channel_nlg.
DR InterPro; IPR003092; TASK_channel.
DR Pfam; PF00520; Ion_trans_1.
DR PRINTS; PRO1333; 2POREKCHANNEL.
DR PRINTS; PRO1584; TASKCHANNEL.
DR PRINTS; PRO1095; TASKCHANNEL.
KW Ionic channel.
FT NON_TER 1
FT 299 299
SQ SEQUENCE 299 AA; 3325 MW; DCD41D8A212939C4 CRC64;

Query Match 63.6%; Score 1298.5; DB 11; Length 301;
Best Local Similarity 85.0%; Pred. No 4.2e-13;
Matches 256; Conservative 6; Mismatches 22; Indels 17; Gaps 2; Variant ";

Q90X34 PRELIMINARY; PRT; 301 AA.

AC Q90X34; DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE TWIK-related acid-sensitive K+ channel sprice variant (TASK1c).
GN KCNK3C.
OS Rattus norvegicus (Rat).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Onya S., Kitsukawa M., Imaizumi Y.;
RA Onya S., Kitsukawa M., Imaizumi Y.;
RA "TWIK-related acid-sensitive K+ channel (TASK1) (KCNK3) splice variant";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB048824; BAB16711.1; -.
DR InterPro; IPR01622; K+channel_2pore.
DR InterPro; IPR00636; M+channel_nlg.
DR InterPro; IPR003092; TASK_channel.
DR Pfam; PF00520; Ion_trans_1.
DR PRINTS; PRO1584; TASKCHANNEL.
DR PRINTS; PRO1095; TASKCHANNEL.
KW IONIC CHANNEL.
FT NON_TER 1
FT 299 299
SQ SEQUENCE 299 AA; 3325 MW; DCD41D8A212939C4 CRC64;

Query Match 65.3%; Score 1333; DB 11; Length 299;
Best Local Similarity 88.9%; Pred. No. 2.5e-16;
Matches 263; Conservative 7; Mismatches 18; Indels 8; Gaps 1;

Q90X34 PRELIMINARY; PRT; 301 AA.

AC Q90X34; DT 01-DEC-2001 (TREMBLrel. 19, Created)

RESULT 3

Q90X34 PRELIMINARY; PRT; 301 AA.

AC Q90X34; DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE TWIK-related acid-sensitive K+ channel sprice variant (TASK1c).
GN KCNK3C.
OS Rattus norvegicus (Rat).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Onya S., Kitsukawa M., Imaizumi Y.;
RA Onya S., Kitsukawa M., Imaizumi Y.;
RA "TWIK-related acid-sensitive K+ channel (TASK1) (KCNK3) splice variant";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB048824; BAB16711.1; -.
DR InterPro; IPR01622; K+channel_2pore.
DR InterPro; IPR00636; M+channel_nlg.
DR InterPro; IPR003092; TASK_channel.
DR Pfam; PF00520; Ion_trans_1.
DR PRINTS; PRO1584; TASKCHANNEL.
DR PRINTS; PRO1095; TASKCHANNEL.
KW IONIC CHANNEL.
FT NON_TER 1
FT 299 299
SQ SEQUENCE 299 AA; 3325 MW; DCD41D8A212939C4 CRC64;

Query Match 63.6%; Score 1298.5; DB 11; Length 301;
Best Local Similarity 85.0%; Pred. No 4.2e-13;
Matches 256; Conservative 6; Mismatches 22; Indels 17; Gaps 2; Variant ";

Q90X34 PRELIMINARY; PRT; 301 AA.

AC Q90X34; DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE TWIK-related acid-sensitive K+ channel sprice variant (TASK1c).
GN KCNK3C.
OS Rattus norvegicus (Rat).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Onya S., Kitsukawa M., Imaizumi Y.;
RA Onya S., Kitsukawa M., Imaizumi Y.;
RA "TWIK-related acid-sensitive K+ channel (TASK1) (KCNK3) splice variant";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB048824; BAB16711.1; -.
DR InterPro; IPR01622; K+channel_2pore.
DR InterPro; IPR00636; M+channel_nlg.
DR InterPro; IPR003092; TASK_channel.
DR Pfam; PF00520; Ion_trans_1.
DR PRINTS; PRO1584; TASKCHANNEL.
DR PRINTS; PRO1095; TASKCHANNEL.
KW IONIC CHANNEL.
FT NON_TER 1
FT 299 299
SQ SEQUENCE 299 AA; 3325 MW; DCD41D8A212939C4 CRC64;

Query Match 63.6%; Score 1298.5; DB 11; Length 301;
Best Local Similarity 85.0%; Pred. No 4.2e-13;
Matches 256; Conservative 6; Mismatches 22; Indels 17; Gaps 2; Variant ";

Q90X34 PRELIMINARY; PRT; 301 AA.

AC Q90X34; DT 01-DEC-2001 (TREMBLrel. 19, Created)

RESULT 4

Q923V6 PRELIMINARY; PRT; 396 AA.

AC Q923V6; DT 01-DEC-2001 (TREMBLrel. 19, Created)

QY 61 ELERVLRKPKHAGVORPAGSTYFAITVITIGYGHAPSTDGGKVCMEVALLGIPL 120
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TAXID=9606;
 DB 61 OLEVILQSESPHRAGVQKMFAGSFYFAITVITIGYGHAPGDAGKACMFAVLGPL 120
 RN [1]
 AC Q9HBC8
 Q9HBC8 PRELIMINARY; PRT; 330 AA.
 DT 01-MAR-2001 (TREMBREL, 16, Created)
 DT 01-MAR-2001 (TREMBREL, 16, Last sequence update)
 DT 01-MAR-2001 (TREMBREL, 20, Last annotation update)
 DT 01-MAR-2002 (TREMBREL, 20, Last annotation update)
 DE Two pore Potassium channel KT3_3 (Tandem pore domain in Potassium channel
 DE TASK-5) (Tandem Acid-sensitive potassium channel TASK5).
 GN KCN15.
 OC Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

RESULT 7

Q8510 PRELIMINARY; PRT; 318 AA.
 ID Q8510; AC Q8510; DT 01-JUN-2002 (TREMBREL, 21, Created)
 DT 01-JUN-2002 (TREMBREL, 21, Last sequence update)
 DT 01-JUN-2002 (TREMBREL, 21, Last annotation update)
 OS Tandem pore potassium channel.
 OC Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TAXID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LONG EVANS TISSUE=BRAIN;
 RA Kawano T., Nakajima S., Nakajima Y.;
 RA "Isolation of rat TASK (KCNK15) cDNA";
 DR Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
 KW Ionic channel.
 SEQUENCE 318 AA: 35651 MW: A0629212F56834ED CRC64;
 Query Match 44.9%; Score 916.5; DB 11; Length 318;
 Best Local Similarity 68.8%; Pred. No. 2.3e-77; Mismatches 185; Conservative 29; Indels 52; Gaps 3; Gaps 3;
 Matches 185; Conservative 29; Mismatches 52; Indels 3; Gaps 3;
 QY 1 MKRQNRVRLTALIVCTFTYLVGAVIDESEPELIERORLRLRQ-PLRARYNLSQGYE 59
 DB 1 MRKQSRARTAHLICLILSILVGAVIDESEPELIERORLRLRQ-SRQLLARKRGRKFRKYRFSADDY 59
 QY 60 EELERVLRKPKHAGVORPAGSFYFAITVITIGYGHAPSTDGGKVCMYALGIP 119
 DB 60 RELERLALQAEPRHAGROWRFAEGSFYFAITVITIGYGHAPSTDGGKVCMYALGIP 119
 QY 120 LTLMFQSLGERINTVILHRAKKGMRRADVSMANAVLIGFFSISTIGIGAAFS 179
 DB 120 LTLMFQSLGERINTVILHRAKKGMRRADVSMANAVLIGFFSISTIGIGAAF 179
 QY 180 HYEWTFPQQAYYCFTLTIGFDYVALQDQALOTQPYQAFSFVYLTGTVIGAFL 239
 DB 180 HEQWTFPQQAYYCFTLTIGFDYVALQDQALOTQPYQAFSFVYLTGTVIGAFL 239
 QY 240 NLVYLRFMNMNAEDEKRAEHRALTRIG 268
 DB 240 NLVYLRFMNMNAEDEKRAEHRALTRIG 268
 QY 240 NLVYLRFMNMNAEDEKRAEHRALTRIG 267
 DB 240 NLVYLRFMNMNAEDEKRAEHRALTRIG 267

RESULT 8

Q9HBC8 PRELIMINARY; PRT; 330 AA.
 ID Q9HBC8; AC Q9HBC8; DT 01-MAR-2001 (TREMBREL, 16, Created)
 DT 01-MAR-2001 (TREMBREL, 16, Last sequence update)
 DT 01-MAR-2002 (TREMBREL, 20, Last annotation update)
 DE Two pore Potassium channel KT3_3 (Tandem pore domain in Potassium channel
 DE TASK-5) (Tandem Acid-sensitive potassium channel TASK5).
 GN KCN15.
 OC Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TAXID=9606;

RESULT 9

Q9HBC8 PRELIMINARY; PRT; 330 AA.
 ID Q9HBC8; AC Q9HBC8; DT 01-MAR-2001 (TREMBREL, 16, Created)
 DT 01-MAR-2001 (TREMBREL, 16, Last sequence update)
 DT 01-MAR-2002 (TREMBREL, 20, Last annotation update)
 DE DT781B1_1 (Two pore potassium channel KT3_3 (LOC64181)) (Tandem acid-sensitive potassium channel TASK5).
 DE DE7781B1_1 OR KCN15.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TAXID=9606;

QY 121 TLVMFQSLGERINTVILHRAKKGMRRADVSMANAVLIGFFSISTIGIGAAFS 180
 DB 121 TLVMFQSLGERINTVILHRAKKGMRRADVSMANAVLIGFFSISTIGIGAAFS 180
 RN [1]
 RA Coetzee W., Rudy B.; RA Coetzee W., Rudy B.;
 RA Vega-Saenz de Miera E.C., Iau D.H.P., Zhadina M., Pountney D.,
 RA "KCNJ2 and KCNJ3 Two Novel Human Two Pore K⁺ Channels Closely Related to TASK1.",
 RA Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RA SEQUENCE FROM N.A.
 RA "ASINOLE 1.", Goodwin P.A., Stanfield P.R.;
 RA "TASK-5, a Novel Member of the Tandem Pore K⁺ Channel Family.",
 RA Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RA SEQUENCE FROM N.A.
 RA Presing-Mueller R., Rajan S., Derszt C.;
 RA "Cloning and sequencing of a novel tandem pore domain potassium channel (TASK-4).",
 RA Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AR257001; AAG33127; 1; -
 DR EMBL; AR336342; AAK37518; 1; -
 DR EMBL; AR294350; AAK37001; 1; -
 DR InterPro; IPR003380; K+channel, 2 pore.
 DR InterPro; IPR001632; K+channel_pore.
 DR InterPro; IPR00636; McCannel_1lg.
 DR InterPro; IPR003092; TASK channel.
 DR Pfam; PRO0520; ion_trans; 1.
 DR PRINTS; PRO1333; 2PORECHANNEL.
 DR PRINTS; PRO1095; TASKCHANNEL.
 KW Ionic channel.
 SEQUENCE 330 AA: 36130 MW: AA2A54D0615BC53C CRC64;
 SQ

Query Match 41.4%; Score 846; DB 4; Length 330;
 Best Local Similarity 64.7%; Pred. No. 9.3e-71; Mismatches 167; Conservative 32; Gaps 59; Indels 0; Gaps 0; Gaps 0;
 Matches 167; Conservative 32; Mismatches 59; Indels 0; Gaps 0; Gaps 0;

QY 1 MKRQNRVRLTALIVCTFTYLVGAVIDESEPELIERORLRLRQ-PLRARYNLSQGYE 60
 DB 1 MRRPSVRAAGLVLTCTYLVGAVIDESEPELIERORLRLRQ-PLRARYNLSQGYE 60
 QY 61 ELERVLRKPKHAGVORPAGSFYFAITVITIGYGHAPSTDGGKVCMYALGIP 120
 DB 61 EELRALQAEPRHAGROWRFAEGSFYFAITVITIGYGHAPSTDGGKVCMYALGIP 120
 QY 121 TLVMFQSLGERINTVILHRAKKGMRRADVSMANAVLIGFFSISTIGIGAAFS 180
 DB 121 TLVMFQSLGERINTVILHRAKKGMRRADVSMANAVLIGFFSISTIGIGAAFS 180
 QY 181 YEHWTFFPQQAYYCFTLTIGFDYVALQDQALOTQPYQAFSFVYLTGTVIGAFN 240
 DB 181 FEGWTFPQQAYYCFTLTIGFDYVALQDQALOTQPYQAFSFVYLTGTVIGAFN 240
 QY 241 LWVLFMNMNAEDEKRAEHRALTRIG 258
 DB 241 LWVLFMNMNAEDEKRAEHRALTRIG 258

QY	1 MKKVNRTISLIVCTFTYLIVGAAVFDALESETERRWERALQDAEDMIRKYNISOEDFK	Db	121 RKPYVAFSEMYLVLGTVIGAFLNLVVLRLFLTANSDEEREGESEGALP-----GNPS 174
QY	61 ELERVLRLKPKHAGQWPRGSEFYFAVIVITGGHAAAPSTOGKVFMCYFLLGIFL 120	QY	276 GGSATTDASSTA - AGGGFRNVYAEVLHFOSMCSCWIKSREKLOYSIPIWIPRL 333
Db	61 VMEVTLKSESHKAGQWNGTGAFTVATLWTTGIGHISTPSTVGGKLTMTGMCYAVGIFL 120	Db	175 SVVHISEEARQVRQRYRREGG-----DLOQSCSCARYQSP - QNFGATLAPQL 223
Db	121 TLVWQOSLGRINTLVYLHRAKGLGMRRADYSANMVALIGFSCISTLCL - GAAFL 178	QY	334 STSDQCVEDSHSPGGGGRYSDTSPRRCJCGSAPRSATSVTSLHSLSTFRGMKRS 393
Db	121 GLWFEQSGER-----AVASSLRKRTVASENDLICV - VTLSSLITRGGAAFL 168	Db	224 HSISCREET-----SPS - TLKNSLFPSPSISSVSPGLHSFGDNHRLMRKS 269
QY	179 SHYRWTTEFOAAYYCFITLTIGRQDVALQDQLOPQYAFSVVILTGTVIGAF 238	QY	394 V 394
Db	169 SKFEGWSYFDSVYCFITLTIGFEDMVALORDNALLRKEVYMFALIFLFGLAIVVAS 228	Db	270 V 270
QY	239 LNLVVLRFMMNADEEKRDAEHRAL-----LTRNGOAGGGGGSAHTDTA 285	QY	
Db	229 LNLVLFYVMTNEDERD - EAQAMQALQVAKLEGDVITSNSLTSGYEGDQSQSLNS 287	Db	
QY	286 SSTAAGGGGRNRYAEVLFQAFOSMC-----LWYKSR -- 320	QY	
Db	288 NTS-----SMCSCHCICLNGNRHKSSNLKNDNAENQYKLROSPT 328	Db	
QY	321 -LOYSIPMILP-RDLS 334	QY	
Db	329 HIRHLLPEVPPMQLN 344	Db	
RESULT 13			
Q9JL57	PRELIMINARY;	PRT;	270 AA.
AC	Q9JL57;	AC	Q9JL57;
DT	01-OCT-2000 (TREMBlrel. 15, Created)	DT	01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT	01-JUN-2002 (TREMBlrel. 21, Last annotation update)	DT	01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE	Potassium channel TASK3 (Fragment).	DE	Tandem acid-sensitive potassium channel TASK5 (Fragment).
GN	KCN9.	GN	KCN15.
OS	Cavia porcellus (Guinea pig).	OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Hystericognathi; Caviidae; Cavia.	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX	NCBI_TAXID=10141;	OX	NCBI_TAXID=10116;
RN	[1]	RN	[1]
SEQUENCE FROM N.A.			
RA	RAJAN S., WISCHMEYER E., LIU G.X., PREISIG-MUELLER R., DAUT J.,	RA	SEQUENCE FROM N.A.
RA	KARSCHIN A., DERTS C.,	RA	STRAIN=WISTAR;
RA	"TASK-3, a novel tandem proe domain acid-sensitive K ⁺ channel. An	RA	PREISIG-MUELLER R., RAJAN S., DERTS C.;
RT	extracellular histidine as pH sensor.",	RT	* Cloning and sequencing of a novel tandem pore domain potassium
RT	J. Biol. Chem. 275:16650-16657 (2000).	RT	channel (TASK-4).";
DR	EMBL: AF212826; AAC63707.1; -.	DR	Submitted (Aug-4-2000) to the EMBL/GenBank/DBJ databases.
DR	InterPro: IPR001622; K+channel_pore.	DR	EMBL: AF294355; AAC9704.1; -;
DR	InterPro: IPR00636; McChannel_lip.	DR	InterPro: IPR001622; K+channel_pore.
DR	Pfam: PF00520; Ion_trans; 1.	DR	Pfam: PF00520; Ion_trans; 1.
DR	PRINTS; PRO1584; TASKCHANNEL.	DR	PRINTS; PRO1584; TASKCHANNEL.
KW	[1]	KW	Ionic channel.
FT	NON_TER 1	FT	NON_TER 1
FT	NON_TER 237	FT	NON_TER 237
SQ	SEQUENCE 237 AA; 26158 MW; 7839915663C98DEF CRC64;	SQ	SEQUENCE 237 AA; 26158 MW;
Query Match			
QY	Best Local Similarity 33.8%; Score 690.5; DB 11; Length 237; Matches 137; Conservative 17; Mismatches 32; Indels 1; Gaps 1;	QY	82 GSFYFAITVITTCGHAAPSTOGKVFMCYFLGIPLYMFOQSGERINTLVRLH 141
Db	1 GSFYFAITVITTCGHAAPGTDSCKVFMCYFLGIPLYMFOQSGERINLALVRCLL 60	Db	142 RAKKGLGMRRADVSANMVLIFFFSCISTLGIGAFAFSHWEHWTFFQAYYCFITLIG 201
QY	NON_TER 1	QY	61 AAKRIGLGRPRHPSAENMVVAGLICAAFLGAFAFREGWTFHAYYCFTLITG 201
Db	NON_TER 1	Db	121 FGDFALORDEALQKPPVYAFSFXLIGLTVIGAFLNLVVLRLA-SAEAPERALR 179
FT	SEQUENCE 270 AA; 29858 MW; 092ABFFC67BC1E56 CRC64;	FT	262 ALTRNG 268
SQ	Best Local Similarity 35.9%; Score 732.5; DB 11; Length 270; Matches 163; Conservative 54.2%; Pred. No. 2.9e-60; Mismatches 163; Indels 33; Gaps 6;	SQ	202 FGDYVALQDKQDQLOPQYAFSVVILTGTVIGAFLNLVVLRLA-SAEAPERALR 179
QY	96 YGHAAPISTOGKVFMCYFLGIPLYMFOQSGERINTLVRLHRAKGLGMRRADYS 155	QY	156 MANMVLIGFFSCISTLGIGAFAFSHWEHWTFFQAYYCFITLIG 215
Db	1 YGHAAPISTOGKVFMCYFLGIPLYMFOQSGERINTLVRLHRAKGLGMRRADYS 60	Db	61 MENMVTVGFFSCMGTICIGAFAFSQCEEMSFHAYYCFTLITGFDYVALQSGALQ 120
QY	216 TQPVYAFSVVILTGTVIGAFLNLVVLRLFMTMNADEKDAEIRALTRNGGAGGGG 275	QY	
RESULT 15			
QY	076790	QY	076790
Db	076790	Db	076790
AC	076790	AC	076790
DT	01-Nov-1998 (TREMBlrel. 08, Created)	DT	01-Nov-1998 (TREMBlrel. 08, Last sequence update)
DT	01-Nov-1998 (TREMBlrel. 08, Last sequence update)	DT	01-Nov-1998 (TREMBlrel. 08, Last sequence update)

OM protein - protein search, using sw model

Run on: July 1, 2003, 15:14:17 ; search time 18 Seconds
(without alignments)
2104.276 Million cell updates/sec

Title: US-09-939-484-4

Perfect score: 2042

Sequence: 1 MRRQNVRTLALIVCTFTYLL. STGLHSLSTFRGIMKRRSSV 394

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0 %

Maximum Match 100 %

Listing first 45 summaries

Database : PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result: #	NO.	Score	Query	Match Length	DB ID	Description
1	846	41.4	JC7703	2	JC7703	RESULT 1 TASK-5 protein - human
2	820	40.2	T43509	2		C;Species: Homo sapiens (man)
3	806.5	39.5	T32347	2		C;Accession: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
4	599	29.3	T19860	2		C;Accession: JC7703
5	599	29.3	T43361	2		R;Kim, D.; Gnatenco, C.
6	320.5	15.7	S65566	2		Biochem. Biophys. Res. Commun. 284, 923-930, 2001
7	307.5	15.1	T28933	2		A;Title: TASK-5, a new member of the tandem-pore K ⁺ channel family
8	293	14.3	T25392	2		A;Reference number: JC7703; MUID:21303050; PMID:11409881
9	276.5	13.5	T68124	2		A;Accession: JC7703
10	275	13.5	T23902	2		A;Molecule type: DNA
11	268	13.1	T30037	2		A;Residues: 1-350 <KIM>
12	262	12.8	T21598	2		A;Cross-references: GB:ALL18522
13	261.5	12.8	T13807	2		A;Comment: This protein, a new member of the tandem-pore K ⁺ channel family with four hormone secretion, but does not produce a functional plasma membrane K ⁺ current by its
14	259.5	12.7	S44635	2		C;Genetics:
15	258.5	12.7	T27681	2		A;Map position: 20q12
16	258	12.6	T23182	2		C;Keywords: transmembrane protein
17	256.5	12.6	T21118	2		F;107-128-/domain: transmembrane segment #status predicted <TMS1>
18	251	12.3	T43364	2		F;129-155-/domain: hydrophobic cytoplasmic linker #status predicted <TMS2>
19	251	12.3	T43363	2		F;156-204-/domain: transmembrane segment #status predicted <TMS3>
20	250	12.2	T43531	2		F;220-240-/domain: transmembrane segment #status predicted <TMS4>
21	248	12.1	T26229	2		Query Match 41.4%; Score 846; DB 2; Length 330;
22	247.5	12.1	T23182	2		Best Local Similarity 64.7%; Pred. No. 1.7e-69; Matches 167; Conservative 32; Mismatches 59; Indels 0; Gaps 0;
23	245	12.0	T27550	2		Qy 1 MRRQNVRTLALIVCTFTYLLGAVALDALESEPELTERQERLRLDQELRARNYLNSOGGYE 60
24	244	11.9	T43393	2		Db 1 MRRPSTRAAGLVLCTLCTYLGVAAVDALESEAERSCRLVQKALRKGFRGEADYR 60
25	243	11.9	T21834	2		Db 61 ELERLALQAEPHRAGROWKFGPSFYFATITVITIGKHAFTGFTDSKVFCHMAYALGIP 120
26	239.5	11.7	T24265	2		Qy 121 TLMFOSLIGERINTTYLLRAKKGIGMRRADVSHANVNLIGEFCISITCIGAAFSH 180
27	235.5	11.5	T27725	2		Db 121 TLVTFOSLIGERLNAAVVRLLAAKCCGLRWTCVSTENLVAGLACATLALGAVAFSH 180
28	234.5	11.5	T43529	2		Qy 181 YEHWTFFQAVYCFITITIGFGDVALQKQALQPOQWYAFSFWYLQGLTVGAFN 240
29	231.5	11.3				Db 181 FEGWTFHAYYCFCITLITLFGFDVALQSLPQAFSFWYLQGLTVGAFN 240
	484	2	T43529			Qy 241 LVVRLFNTMNAEDEKRD 258
						Db 241 LVVRLFELVASADWPERA 258
						RESULT 2

T45509 probable potassium channel chain n2P38 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000

C:Accession: T45509

R:Wang, Z.W.; Salkoff, L.

submitted to the EMBL Data Library, August 1998

A:Description: Potassium channels in *C. elegans*.

A:Reference number: T45509

A:Status: preliminary; translated from GB/EMBL/DDJB

A:Molecule type: mRNA

A:Residues: 1-329 <WAN>

A:Cross-references: EMBL:AF083652; PIDN: AAC32863.1

Query Match 40.2%; Score 830; DB 2; Length 329;

Best Local Similarity 40.3%; Pred. No. 4e-67; Mismatches 54; Indels 84; Gaps 7;

Matches 172; Conservative 54; MisMatches 84; Indels 46; Gaps 7;

Db 1 MKNQNRVTLALIVCTFLVGAVALDSEPELIE-----RQRLRQELQRLR 60

Db 1 MKRNIRITLISLIVCTLTLIVLGAVALDALETEENILQRLQYRERKLTQKVNMSNADYE 60

Qy 61 ELERVVLRLKPHAGVQWRFAGSFYFAITWITITGYGHAPSTDGKVFVCMYALLGIPL 120

Db 61 ILEATIVKSRVPHAGYQWKFSGAFYFAITWITITGYGHAPSTDGKVFVCMYALLGIPL 120

Qy 121 TLYMFQSLGERINTLVLRLHAKKGLMRADYSMANMVLFPGFSCISTICL-----GAFAF 178

Db 121 GLIMFQSLGERMVFIAAKLRFIRRAAG-KQPVITSSDIL---FCTGNGGLIFGGAFMF 177

Qy 179 SHYEHWTFFQAYYCFCITLTGFGDYVALQKQDQALQTOPQYVAFSFVYLGLTVGF 238

Db 178 SSYENWNTYEDAVVYCFVLTTCITGFGDYVALQKQDSLQPEVYFFSLVFLRGLTVISA 237

Qy 239 LNLVLRFLFTMNADEKDAEHRAL---LTRNGQAGGGGGSAHTTDTASSTAAGGG 294

Db 238 MNLLVLRFLFTMNADEKDAEHRAL---LTRNGQAGGGGGSAHTTDTASSTAAGGG 292

Qy 295 GFRNVVAEVLFHQSMCSCILWYKSVREKQYSIPMTIPDLSSTDICVEQSHSSPGG 350

Db 293 -----CSC-YQLPDEKLHR-----HRKTEPHGG 316

RESULT 3

T32347 outward rectifier potassium channel homolog twk-23 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C:Accession: T32347

R:Murray, J.; Wohldmann, P.; O'Neal, D.

submitted to the EMBL Data Library, September 1997

A:Description: The sequence of C. elegans cosmid F34D6.

A:Reference number: Z21153

A:Accession: T32347

A:Status: preliminary; translated from GB/EMBL/DDJB

A:Molecule type: DNA

A:Residues: 1-336 <MUR>

A:Cross-references: EMBL:Z70266; PIDN:CAA94204.1; GSPDB:GN00028; CESP:C40C9.1

A:Experimental source: clone C40C9

A:Genes: CESP:C40C9.1

A:Map position: X

A:Introns: 34/1; 60/2; 98/1; 145/3; 160/3; 181/1; 204/1; 252/2; 279/2; 306/3

Query Match 29.3%; Score 599; DB 2; Length 334;

Best Local Similarity 46.1%; Pred. No. 6.5e-47; Mismatches 119; Conservative 46; MisMatches 81; Indels 12; Gaps 3;

Matches 119; Conservative 46; MisMatches 81; Indels 12; Gaps 3;

Db 4 QNVRTALIVCTFLVGAVALDSEPELIERQRLRQELRQELRQELRQELRQELR 63

Db 7 KSARALLLSTFMYLFLGAMVWDFKLESEKDWTWDRDETERIDRKLHKYNSFERSDHLFL 66

Qy 64 RVLRLKHKAGVQWRFAGSFYFAITWITITGYGHAPSTDGKVFVCMYALLGIPL 123

Db 67 ALAKLSITQOQAGYQWKFSGAFYFAITWITITGYGHAPSTDGKVFVCMYALLGIPL 126

Db 124 MFQSLGERINTLVLRLHAKKGLMR---RADVSMANVL---IGFFSCISTICLICA 175

Db 127 MFQSLGERINTLVLRLHAKKGLMR---RADVSMANVL---IGFFSCISTICLICA 182

Qy 176 AAFSHWHTFFQAYYCFCITLTGFGDYVALQKQDQALQTOPQYVAFSFVYLGLTVI 235

Db 183 YMFTHTKWSIFDAYFCMITSFSTGFDLVPQVNLQDOPLYWFTATMFLIGLAVF 242

Qy 236 GAFLNLVLRFLFTMNAED 253

Db 243 SACVNLVLGFMASNADE 260

RESULT 4

T19860 hypothetical protein C40C9.1 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C:Accession: T19860

R:Hembry, C.

submitted to the EMBL Data Library, March 1996

A:Reference number: Z19188

A:Status: preliminary; translated from GB/EMBL/DDJB

A:Molecule type: DNA

A:Residues: 1-334 <WIL>

A:Cross-references: EMBL:Z70266; PIDN:CAA94204.1; GSPDB:GN00028; CESP:C40C9.1

A:Experimental source: clone C40C9

A:Genes: CESP:C40C9.1

A:Map position: X

A:Introns: 34/1; 60/2; 98/1; 145/3; 160/3; 181/1; 204/1; 252/2; 279/2; 306/3

Query Match 29.3%; Score 599; DB 2; Length 334;

Best Local Similarity 46.1%; Pred. No. 6.5e-47; Mismatches 119; Conservative 46; MisMatches 81; Indels 12; Gaps 3;

Matches 119; Conservative 46; MisMatches 81; Indels 12; Gaps 3;

Db 4 QNVRTALIVCTFLVGAVALDSEPELIERQRLRQELRQELRQELRQELR 63

Db 7 KSARALLLSTFMYLFLGAMVWDFKLESEKDWTWDRDETERIDRKLHKYNSFERSDHLFL 66

Qy 64 RVLRLKHKAGVQWRFAGSFYFAITWITITGYGHAPSTDGKVFVCMYALLGIPL 123

Db 67 ALAKLSITQOQAGYQWKFSGAFYFAITWITITGYGHAPSTDGKVFVCMYALLGIPL 126

Db 124 MFQSLGERINTLVLRLHAKKGLMR---RADVSMANVL---IGFFSCISTICLICA 175

Db 127 MFQSLGERINTLVLRLHAKKGLMR---RADVSMANVL---IGFFSCISTICLICA 182

Qy 176 AAFSHWHTFFQAYYCFCITLTGFGDYVALQKQDQALQTOPQYVAFSFVYLGLTVI 235

Db 183 YMFTHTKWSIFDAYFCMITSFSTGFDLVPQVNLQDOPLYWFTATMFLIGLAVF 242

Qy 236 GAFLNLVLRFLFTMNAED 253

Db 243 SACVNLVLGFMASNADE 260

RESULT 5

T43361 probable potassium channel chain n2P20 - *Caenorhabditis elegans*

A;Accession: T25392
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-393 <WIL>
 A;Cross-references: EMBL:Z2813; PIDN:CA07286.1; GSPDB:GN00021; CESP:T28A8.1
 A;Genetics: CESP:T28A8.1
 A;Map position: 3
 A;Introns: 73/1; 112/3; 179/2; 209/3; 287/2; 310/3; 364/2

 Query Match 14.3%; Score 293; DB 2; Length 393;
 Best Local Similarity 26.6%; Pred. No. 7-7e-19;
 Matches 78; Conservative 57; Mismatches 96; Indels 62; Gaps 9;

 Qy 9 LALIVCTFTYLLGAAVDALESEPEL-----IERTQRELRO----- 45
 Db 15 VSLIVLVSIVYVGAFGLYVQLEPNEVERARNIEFHNFHMRKGSARLDSAWKFRGLESIDSISDLESASKNQSS 428

 Qy 46 -QELRARY--NLSQGGYEELELRVVLRLKKPHAG---WQWRFASGFYFAITIVITIGY 97
 Db 75 VEDLAVKVVDVNTRILFEAFDFDHCIGAHLRPGGEDEDYNWNTWTALEFTTILITIGY 134

 Qy 98 HAAPSTDGCKVFCMFYALIGIPLTLMQFQSLGERI-NWLVRLHLR----- 142
 Db 135 NLTPVTGKGKULCILYALLEGVPFLITYADIGKFLSENIVQLYTWIKRLREKSKQKYSV 194

 Qy 143 -AKKGGLGMRRADVS---WANHVLIGETSCC---STLIGAFAFSHYHWTFOAYYCC 194
 Db 195 ISSDDKDKNEKGNDLHNLVYIPIFLIVAILIISYTFGAVVLSWGMGDFTSF 254

 Qy 195 ITLTIGCFDYVALQDQALQIQPOQYVAESFWVLTGIVIGAFLNLYVLRFM 247
 Db 255 ITMWTIVGRDIVPLKR-----EYVILDCYIIIGLISITMCIDLVGQYI 299

 RESULT 9
 H88124 protein T12C9.3 [imported] - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 10-May-2001 #sequence_revision 10-May-2001
 C;Accession: H88124
 Science 282, 2012-2018, 1998
 A;Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology
 A;Reference number: A75000; MURG:9905613; PMID:9851916
 A;Note: see website: wustl.edu/gsc_elegans and www.sanger.ac.uk/Projects/C_elegans
 A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
 A;Accession: H88124
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1910 <STR>
 A;Cross-references: GB:chr_II; PIDN:AC71141.1; PID:91086770; GSPDB:GN00020; CESP:T12C9.3
 A;Note: proline rich
 C;Genetics:
 A;Gene: T12C9.3
 A;Map position: 2

 Query Match 13.5%; Score 276.5; DB 2; Length 1910;
 Best Local Similarity 23.3%; Pred. No. 1.7e-16;
 Matches 80; Conservative 49; Mismatches 107; Indels 107; Gaps 8;

 Qy 4 QNVRTLA-----LIVCTFTYLLGAAVDALES-EPELTERQRLRQELRARNY 53
 Db 189 QNTRKVKALPHILVAVVCCIVATIGAWIYFTLESPNDRLIKETGRITIAEMRSNLVY 248

 Qy 54 LS----- 67
 Db 249 INNNEKEWPKEDIEKELMLYSEKLYKAPEKQY'YRISDVRTIGFEGRSYYEADETGGDSE 308

 Qy 68 RLPHKAC-----WQWRFASGFYFAITIVITIGYGAAPSTDEGKVFEMYALGI 118
 Db 309 RKKRHRHGNRGRDGSKEKWTISSLFFATTMATICGGNTPVTPGLRACVLFLALFGA 368

 RESULT 10
 T23907 hypothetical protein R04F11.4 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C;Accession: T23907
 R. Harris, B.
 submitted to the EMBL Data Library, June 1996
 A;Reference number: Z19816
 A;Accession: T23907
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-524 <WIL>
 A;Cross-references: EMBL:Z74475; PIDN:CAA98957.1; GSPDB:GN00023; CESP:R04F11.4
 A;Experimental source: clone R04F11
 C;Genetics:
 A;Gene: CESP:R04F11.4
 A;Map position: 35/3; 83/2; 131/1; 170/1; 261/1; 306/1; 338/1; 369/1; 489/2

 Query Match 13.5%; Score 275; DB 2; Length 524;
 Best Local Similarity 23.9%; Pred. No. 4.8e-17;
 Matches 88; Conservative 38; Mismatches 92; Indels 150; Gaps 9;

 Qy 11 LIVCTFTYLLGAAVDALESEPELTERQRLRQELRARY----- 52
 Db 18 LVLSISGYRLIGAIYCFHAEVKPEQQLRNETSRRIQELKRNVMDQLWMSNNGTYASTWR 77

 Qy 53 NLSQGGYEELELRVVL-----RKH-----KAGVWQWRFASGFYFAITIVITIGYHAP 101
 Db 78 QTANIGMDLIELRDFWDYDTRNYMPDDYVGDGPKIWSFMSIFFSWTAITIGHIVP 137

 Qy 102 STQGKVFCMFYALIGIPLTLMQFQSLGERI-NWLVRLHLR----- 136
 Db 138 RTDEGRVATIYALIGIPLVLTADIGRFATYIKLHLHGYMAVMSFTNSCLRKICWA 197
 Qy 137 -----RY-----LHRKK-----GLGMR----- 150
 Db 198 CCWIRPRRHPMPTELLQRTQKPNNNPVTATAASAGGGTGRKKQQDRDNVSDAG 257

 Qy 151 ----- 174
 Db 258 TFDNISEINQSEGGENENEGEREERQIQEDPSNHEKRVSVLFLIMIGY-----VAGG 311

 Qy 175 AAQFSHYHWTFOQAYYCFITLTIGGDFYVALQDQALQTOPOQYVAESFWVLTGIVT 234
 Db 312 AYTWRWWBWTTEAFAYFCFVTTIGFGRDIVPANVD-----WLPATLAYIVFGLI 363

 Qy 235 IGAFLNLV 242
 Db 364 TTMCIDLV 371

 RESULT 11
 T30037 hypothetical protein F20A1.7 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C;Accession: T30037

R; Gattung, S.; Wu, X.
Submitted to the EMBL Data Library, March 1996
A; Description: The sequence of *C. elegans* cosmid F20A1.
A; Reference number: 220726
A; Accession: T20037
A; Status: preliminary; translated from GB/EMBL/DDJB
A; Molecule type: DNA
A; Residues: 1-1539 <CAT>
A; Cross-references: EMBL:053150; PIDN:AA96127_1; GSPDB:GN00023; CESP:F20A1.7
A; Experimental source: strain Bristol N2; clone F20A1
C; Genetics:
A; Gene: CESP:F20A1.7
A; Map position: 5
A; Introns: 19/3; 41/2; 71/2; 110/3; 135/2; 190/1; 246/1; 287/3; 491/3; 598/2; 983/2; 110
Query Match
Best Local Similarity 13.18; Score 268; DB 2; Length 1539;
Matches 96; Conservative 60; Mismatches 126; Indels 108; Gaps 13;
Qy 8 TALIIVCTFTYLIVGAADFALDALESEPELIERO-----RUELQOELRA-RYNUSQGG 58
Db 88 TEKLILIGLYRPIGAHFMVLEVPDLEAREDGFHQRRKIREVMVNLRAFYDNRDR 147
Qy 59 YERBLERYVLRPLPKHACQ-----WRFAGSFYFAITVITIGYHAPSPDGKRYFCM 111
Db 148 EERWKHAKILKFE-EDIGLEEPVIETWTFWMSFLYAGCTIFTIGYGNACKTRAGQATM 206
Qy 112 FVALLGIPPLTUMFQSU-----GERI----- 132
Db 207 VFAVFGIPIMLWMLTSINFLWKWIKLITNGSDMTLYIGVRLGTVIRODEVQKRLRYT 266
Qy 133 --NTLYYLL--HRAKKGLGMRRADYSMANN----- 131
Db 267 KLAKTMRWKLKRGASSIATSNSENRNLNSTPDEEEERIHQDPFLPSLTLIAVWAI 326
Qy 172 CIGAAAFSHYEHMTFFQAYYCPITLTIGECDYVALQKDQDQLQTOPQYQVARSFWYITG 231
Db 327 ILSAAVFCFLFEDWTFPSYFCFISLTITGLD-----VTPANPEYIMTFGVVING 378
Qy 232 LWTIGATNLVLYLREMONTNAEDEKRDARHALLTRNGOAGGGGGGSAHTDTASSAA 291
Db 379 LSMLTVCDVLOERLQKQYM-----ALLQKLITTEYMAVKSG-----DPNAASAMMA 425
Qy 292 GGGG-----FRNVAEVL-HFOSMCs 311
Db 426 GFGQGRAKELMLPLISKNGBKAQVNDKEKODCS 455
RESULT 12
T21598
hypothetical protein F31D4.7 - *Caenorhabditis elegans*
C; Species: *Caenorhabditis elegans*
C; Date: 15-oct-1999 #sequence_revision 15-oct-1999 #text_change 15-oct-1999
C; Accession: T21598
R; Mortimore, B.
A; Submitted to the EMBL Data Library, March 1997
A; Reference number: 219447
A; Accession: T21598
A; Status: preliminary; translated from GB/EMBL/DDJB
A; Molecule type: DNA
A; Residues: 1-443 <WIL>
A; Cross-references: EMBL:292832; PIDN:CA007375_1; GSPDB:GN00023; CESP:F31D4.7
A; Experimental source: clone F31D4
C; Genetics:
A; Gene: CESP:F31D4.7
A; Map position: 5
A; Introns: 13/3; 90/2; 149/1; 222/3; 290/3
Query Match 12.8%; Score 262; DB 2; Length 443;
Best Local Similarity 25.0%; Pred. No. 6.1e-16;
Matches 78; Conservative 55; Mismatches 113; Indels 66; Gaps 9;
Qy 111 LIVCTFTYLIVGAADFALDALESEPELIERO-----RUELQOELRA-RYNUSQGG 56

Db 17 LIVELIVCISGGLFLWNLIEPYOSELRAWHKIKIENNTRDAMMKKIFNNSDLYI 76
Qy 57 ----->GGYELLERVVRKPKHAGVOMWRFAGSFYFAITVITIGYHAA 100
Db 77 KNTVSQRTTFFLEEGSYEN---QLGVKAQOKMDFWNARVFLGTCITIGYHII 132
Qy 101 PSTDGGKVFCMRYVALQGSIPLTLMWFOSLGERINTLVRLHRAKKG----- 147
Db 133 PWDAGRMLTMFLAFGKIPMLVLODFGKLITMKPWFOTKLRMRRIMRCCTKOPIE 192
Qy 148 -----GMRRAVMSMANNL-IGFCSISTLIGAAESHYH-WTFQAVYCFILTT 199
Db 193 EMKEIERQERHLDIFDPLPVGIALTMWTFCSFLVSDHNWTLLESFEPFTSLT 252
Qy 200 IGRGDYVYALQKDOALQTOPOQYAFASFVYLITGIVGIAFLNLYVLRMT--MNAEDEKR 256
Db 253 VGLDGV-----PSPLRULITMCFPLVGLSLSWVNLQANKSTYEARNEDEKT 304
Db 305 PHHQTLPTSLG 316

RESULT 13
T13807
potassium channel protein - fruit fly (*Drosophila melanogaster*)
C; Species: *Drosophila melanogaster*
C; Accession: T13807
C; Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
R; Goldstein, S.A.; Price, L.A.; Rosenthal, D.N.; Pausch, M.H.
Proc. Natl. Acad. Sci. U.S.A. 93, 12565-12561, 1996
A; Title: ORK1, a potassium-selective leak channel with two pore domains cloned from Drosophila melanogaster
A; Reference number: 217770; MURID:97075152; PMID:8917578
A; Accession: T13807
A; Status: preliminary; translated from GB/EMBL/DDJB
A; Molecule type: mRNA
A; Residues: 1-1001 <GOI>
A; Cross-references: EMBL:055321; NID:93808067; PID:93808068; PIDN: AAC69250.1
C; Genetics:
A; Gene: ORK1
A; Cross-references: FLYBase:FBgn0017561
A; Map position: 1

Query Match 12.8%; Score 261.5; DB 2; Length 1001;
Best Local Similarity 25.0%; Pred. No. 1.8e-15;
Matches 69; Conservative 65; Mismatches 107; Indels 35; Gaps 8;

Qy 7 RTALIIVCTFTYLIVGAADFALDALESEPELIERORRLEQOELRARNRYSQGGYEL--- 62
Db 5 RWLILFVFTYSLMLVGAIIYVHIEHGEEKS-----RAEQRKQIAINEYELIEGLDKN 58
Qy 63 ---ERVVLRL---KP-----HKAGVWRFAGSFYFAITVITIGYHAA 106
Db 59 TTTGDEIQLRISPCDKVTPYDOPPTWYHAFEFATVCSTVYGGNISPTTFFG 118
Qy 107 KVFCMFYALGIPPLTLMWFOSLGERINTLVRLHRAK-----GLGRADYSMANNL 161
Db 119 RMMIAIAVSGIVPGLGILFAGLGEFGRFEIIRRKKYKSTDMHVPPOLGLITV 178
Qy 162 IGFSCIST-LCIGAAAFSHYEHMTFFQAYYCFITLTIGFDDYV-ALQKQDQALQPO 219
Db 179 IALPGIALFLLPSWVFTENPPYSLPSVYVTTGFGDYYPTFGANQPKERFGG 238
Qy 220 YVAFSFVWVLTGIVLWIGFLNVLWLFRTMNAEKA 255
Db 239 FVYVQIVVWFFISLGYL--VMIMTFTRGQSKK 272

RESULT 14
S14635 f2b7.7 Protein - *Caenorhabditis elegans*
C; Species: *Caenorhabditis elegans*

GenCore version 5.1.6
 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 1, 2003, 15:15:48 ; Search time 26 Seconds
 (without alignments)
 1661.571 Million cell updates/sec

Title: US-09-939-484-4

Perfect score: 2042

Sequence: 1 MRQONVRLALIVCTFTYLL.....STGLHSLSTFRGLMKRRSSV 394

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 424699 seqs, 109646833 residues

Total number of hits satisfying chosen parameters: 424699

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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14: /cgn2_6/podata/1/pubpa/US60_PUBCOMB_pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2042	100.0	394	10 US-09-939-483-4
3	2042	100.0	394	10 US-09-939-484-15
4	1819	89.1	405	10 US-09-939-484-5
5	1819	89.1	405	10 US-09-939-483-5
6	1278	62.6	258	10 US-09-746-491-61
7	1116	54.7	374	10 US-09-798-584-1
8	1069.5	52.4	365	10 US-09-746-491-60
9	846	41.4	330	10 US-09-746-491-59
10	838	41.0	330	10 US-09-746-491-58
11	838	41.0	393	10 US-09-746-491-22
12	774	37.9	279	10 US-09-761-34389
13	370	10	370	10 US-09-939-484-8
14	370	10	370	10 US-09-939-483-8
15	369	18.1	411	10 US-09-828-746-5
16	363	17.8	411	9 US-10-121-746-83
17	363	17.8	411	10 US-09-828-746-2
18	361	17.7	294	9 US-10-121-966-2
19	349.5	17.1	526	10 US-09-729-920-4
20	349.5	17.1	538	10 US-09-729-920-5
21	349.5	17.1	543	10 US-09-729-920-2
22	329.5	16.1	392	10 US-09-747-835A-55
23	329.5	16.1	393	9 US-10-243-035-2
24	329.5	16.1	419	10 US-09-828-035-2
25	329.5	14.5	1314	10 US-10-205-823-190
26	320.5	15.7	336	10 US-09-939-484-2
27	320.5	15.7	336	10 US-09-939-483-2
28	320.5	15.7	499	10 US-09-735-169A-2
29	319	15.6	499	10 US-09-735-171A-2
30	319	15.6	499	10 US-09-735-171A-2
31	295.5	14.5	313	10 US-09-735-169A-8
32	295.5	14.5	313	10 US-09-735-171A-8
33	294.5	14.4	336	10 US-09-735-169A-5
34	294.5	14.4	332	10 US-09-735-171A-5
35	294.5	14.4	383	10 US-09-939-484-7
36	190.5	9.3	383	10 US-09-939-483-7
37	190.5	9.3	383	10 US-09-939-483-7
38	179	8.8	39	10 US-09-746-491-63
39	176.5	8.6	107	10 US-09-828-746-4
40	156	7.6	347	10 US-09-939-484-6
41	156	7.6	41	156 US-09-939-483-6
42	131.5	6.4	646	9 US-10-121-746-10
43	123.5	6.0	223	9 US-10-162-012-9
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45	5.8	9	988	9 US-09-875-321-12

Database : Published Applications AA:*

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14: /cgn2_6/podata/1/pubpa/US60_PUBCOMB_pep:*

RESULT 1

US-09-939-484-4

Sequence 4, Application US/09939484

Patent No. US2002032322A1

GENERAL INFORMATION:

APPLICANT: Duprat, Fabrice

APPLICANT: Léage, Florian

APPLICANT: Fink, Michel

APPLICANT: Lazdunski, Michel

TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING AND USE, ESPECIALLY FOR THE SCREENING OF DRUGS

FILE REFERENCE: 1201-CIP-DIV-00

CURRENT APPLICATION NUMBER: US/09/939,484

PRIOR APPLICATION NUMBER: 09/144,914

PRIOR FILING DATE: 1998-09-01

PRIOR APPLICATION NUMBER: 08/749,816

PRIOR FILING DATE: 1996-11-15

PRIOR APPLICATION NUMBER: 60/095,234

PRIOR FILING DATE: 1998-08-04

PRIOR APPLICATION NUMBER: FR 96/01565

PRIOR FILING DATE: 1996-02-08

NUMBER OF SEQ ID NOS: 24

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 4

LENGTH: 394

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: TASK

US-09-939-484-4

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Matches 394; Conservative 0; Sequence 5, Appli

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Query Match Similarity 100.0%; Score 2042; DB 10; Length 394; Best Local Similarity 100.0%; Pre 2e-082;

; ORGANISM: Mus musculus
; US-09-746-491-61

Query Match 62.6%; Score 1278; DB 10; Length 258;
Best Local Similarity 96.1%; Pred. No. 2.5e-11; 5; Mismatches 248; Conservative 5; Indels 0; Gaps 0;

Qy 1 MKRQNVRTALIVCTFTYLGVAAVDALESEPLIERQRLRQELARYNLSQGGE 60
Db 1 MKRQNVRTALIVCTFTYLGVAAVDALESEPLIERQRLRQELARYNLSQGGE 60
Qy 61 ELEVVLRLPKPHKGQWQRFAGSFYFAITVITIGYGHAPSTDGKVFQCMFVALGLPL 120
Db 61 ELEVVLRLPKPHKGQWQRFAGSFYFAITVITIGYGHAPSTDGKVFQCMFVALGLPL 120
Qy 121 TLVMFQSLGERINLVRLHRAKKGLGRADVSMMANVLGFESCISTLCGAFAFSH 180
Db 121 TLVMFQSLGERINLVRLHRAKKGLGRADVSMMANVLGFESCISTLCGAFAFSH 180
181 YERHTFFQAVYCYCTIFTLIGFGDYVALQKDQALQTQPOYVAFSFVYITLGTVIGAFN 240
Qy 241 LVVLFRTMNAEDKRD 258
Db 241 LVVLFRTMNAEDKRD 258

RESULT 7
US-09-798-584-1
; Sequence 1, Application US/09798584
; Patent No. US20020102676A1
; GENERAL INFORMATION:
; APPLICANT: Mu, David
; APPLICANT: Powers, Scott
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: A No. US20020102676A1. Potassium Channel Protein
; FILE REFERENCE: 018781-004100US
; CURRENT APPLICATION NUMBER: US/09/798,584
; CURRENT FILING DATE: 2001-03-03
; PRIOR APPLICATION NUMBER: US 60/186,951
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: OTHER INFORMATION: human KCNB (Potassium channel expressed in Breast)
; US-09-798-584-1

Query Match 54.7%; Score 1116; DB 10; Length 374;
Best Local Similarity 59.0%; Pred. No. 5.6e-95; 6; Mismatches 233; Conservative 44; Indels 22; Gaps 5;

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Best Local Similarity 59.0%; Pred. No. 5.6e-95; 6; Mismatches 233; Conservative 44; Indels 22; Gaps 5;

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Db 1 MKRQNVRTALIVCTFTYLGVAAVDALESEPLIERQRLRQELARYNLSQGGE 60
Qy 61 ELEVVLRLPKPHKGQWQRFAGSFYFAITVITIGYGHAPSTDGKVFQCMFVALGLPL 120
Db 61 ELEVVLRLPKPHKGQWQRFAGSFYFAITVITIGYGHAPSTDGKVFQCMFVALGLPL 120
Qy 121 TLVMFQSLGERINLVRLHRAKKGLGRADVSMMANVLGFESCISTLCGAFAFSH 180
Db 121 TLVMFQSLGERINLVRLHRAKKGLGRADVSMMANVLGFESCISTLCGAFAFSH 180
181 YERHTFFQAVYCYCTIFTLIGFGDYVALQKDQALQTQPOYVAFSFVYITLGTVIGAFN 240
Qy 241 LVVLFRTMNAEDKRD 258
Db 241 LVVLFRTMNAEDKRD 258

RESULT 8
US-09-746-491-60
; Sequence 60, Application US/09746491
; Patent No. US2002013720A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: No. US2002013720A1. Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 1596-621
; CURRENT APPLICATION NUMBER: US/09/746,491
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: USN 60/171,329
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 60
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Cavia porcellus
; US-09-746-491-60

Query Match 52.4%; Score 1069.5; DB 10; Length 365;
Best Local Similarity 57.1%; Pred. No. 1.2e-91; 6; Mismatches 226; Conservative 43; Indels 33; Gaps 6;

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Db 1 MKRQNVRTALIVCTFTYLGVAAVDALESEPLIERQRLRQELARYNLSQGGE 60
Qy 61 ELEVVLRLPKPHKGQWQRFAGSFYFAITVITIGYGHAPSTDGKVFQCMFVALGLPL 120
Db 61 ELEVVLRLPKPHKGQWQRFAGSFYFAITVITIGYGHAPSTDGKVFQCMFVALGLPL 120
Qy 121 TLVMFQSLGERINLVRLHRAKKGLGRADVSMMANVLGFESCISTLCGAFAFSH 180
Db 121 TLVMFQSLGERINLVRLHRAKKGLGRADVSMMANVLGFESCISTLCGAFAFSH 180
181 YERHTFFQAVYCYCTIFTLIGFGDYVALQKDQALQTQPOYVAFSFVYITLGTVIGAFN 240
Qy 241 LVVLFRTMNAEDKRD 258
Db 241 LVVLFRTMNAEDKRD 258

RESULT 9
US-09-46-491-59
; Sequence 59, Application US/09746491
; Patent No. US2002013720A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: No. US2002013720A1. Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-621

Db 241 LVVLFRTMNAEDKRD 258
Qy 301 -AEVHFQNSCSCUWKSREKQSIQPMIPRDLSTSDTCVQSHSSPGGGYSDTFSR 359
Db 287 KADPFDLQSCSCTCYRSQD--YGGRSYAPONSKAKPHFHSISKIEEISPSTIK 343
Qy 360 RCLCSEGAPRSAISSVSTGHLSLSTFRGLMKRSSV 394
Db 344 NSLFP---SPISSPGHLSTDHQRLMKRSSV 374

CURRENT APPLICATION NUMBER: US/09/746,491
 CURRENT FILING DATE: 2000-12-20
 PRIOR APPLICATION NUMBER: USN 60/171,329
 PRIOR FILING DATE: 1999-12-21
 NUMBER OF SEQ ID NOS: 72
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 59
 LENGTH: 330
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-746-491-59

Query Match 41.4%; Score 846; DB 10; Length 330;
 Best: Local Similarity 64.7%; Pred. No. 7.7e-71; Matches 167; Conservative 32; Mismatches 59; Indels 0; Gaps 0;
 Qy 1 MKRQNYRTLALIYCTTYLVAAYVDALESEPELTERORLELROELRARNLNSGGYE 60
 Db 1 MRRPSVRAAGLVLCTLYLVAAYVDALESEPELTERORLELROELRARNLNSGGYE 60
 Qy 61 ELERVVLRLKHKAGQWRFAGSFYAITVITIGHAAFTSTGGKVFCMFYALIGIPL 120
 Db 61 ELERLALQAEPRHAGROWKFGPSFYAITVITIGHAAFTSTGGKVFCMFYALIGIPL 120
 Qy 121 TLYMFOSLGERINTLVYLHRAKKGIGMRRADVSAMMVNLIGFFCISTICIGAAFSH 180
 Db 121 TLVTFOSLGERLNAVVRLLIAAKCCLGLRVCSTENLVAAGLCAATLALGAVAFSH 180
 Qy 181 YEHWTFFQAYYCFTLTIGFGDYVALQKDALQTOPQYVAFSFVYILGLTIGAFLN 240
 Db 181 FEGWTFPHAYYCFTLTIGFGDYVALQKDALQTOPQYVAFSFVYILGLTIGAFLN 240
 Qy 241 LVVLREMTMNAEDEKRA 258
 Db 241 LVVLRELVASADWPERAA 258

RESULT 10
 US-09-746-491-58
 ; Sequence 58, Application US/09746491
 ; Patent No. US20020137202A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Burgess, Catherine E.
 ; TITLE OF INVENTION: No. US20020137202A1el Proteins and Nucleic Acids Encoding Same
 ; FILE REFERENCE: 15966-621
 ; CURRENT APPLICATION NUMBER: US/09/745,491
 ; CURRENT FILING DATE: 2000-12-20
 ; PRIOR APPLICATION NUMBER: USN 60/171,329
 ; NUMBER OF SEQ ID NOS: 72
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO: 22
 ; LENGTH: 393
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: VARIANT
 ; LOCATION: (340)
 ; OTHER INFORMATION: Wherein Xaa is any amino acid as defined in the
 ; OTHER INFORMATION: specification
 ; US-09-746-491-22

Query Match 41.0%; Score 838; DB 10; Length 393;
 Best: Local Similarity 64.3%; Pred. No. 5.4e-70; Matches 166; Conservative 32; Mismatches 60; Indels 0; Gaps 0;
 Qy 1 MKRQNYRTLALIYCTTYLVAAYVDALESEPELTERORLELROELRARNLNSGGYE 60
 Db 1 MRRPSVRAAGLVLCTLYLVAAYVDALESEPELTERORLELROELRARNLNSGGYE 60
 Qy 61 ELERVVLRLKHKAGQWRFAGSFYAITVITIGHAAFTSTGGKVFCMFYALIGIPL 120
 Db 61 ELERLALQAEPRHAGROWKFGPSFYAITVITIGHAAFTSTGGKVFCMFYALIGIPL 120
 Qy 121 TLYMFOSLGERINTLVYLHRAKKGIGMRRADVSAMMVNLIGFFCISTICIGAAFSH 180
 Db 121 TLVTFOSLGERLNAVVRLLIAAKCCLGLRVCSTENLVAAGLCAATLALGAVAFSH 180
 Qy 181 YEHWTFFQAYYCFTLTIGFGDYVALQKDALQTOPQYVAFSFVYILGLTIGAFLN 240
 Db 181 FEGWTFPHAYYCFTLTIGFGDYVALQKDALQTOPQYVAFSFVYILGLTIGAFLN 240
 Qy 241 LVVLREMTMNAEDEKRA 258
 Db 241 LVVLRELVASADWPERAA 258

RESULT 10
 US-09-746-491-58
 ; Sequence 58, Application US/09746491
 ; Patent No. US20020137202A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Burgess, Catherine E.
 ; TITLE OF INVENTION: No. US20020137202A1el Proteins and Nucleic Acids Encoding Same
 ; FILE REFERENCE: 15966-621
 ; CURRENT APPLICATION NUMBER: US/09/745,491
 ; CURRENT FILING DATE: 2000-12-20
 ; PRIOR APPLICATION NUMBER: USN 60/171,329
 ; NUMBER OF SEQ ID NOS: 72
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO: 22
 ; LENGTH: 393
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: VARIANT
 ; LOCATION: (340)
 ; OTHER INFORMATION: Wherein Xaa is any amino acid as defined in the
 ; OTHER INFORMATION: specification
 ; US-09-746-491-22

Query Match 41.0%; Score 838; DB 10; Length 330;
 Best: Local Similarity 64.3%; Pred. No. 4.3e-70; Matches 166; Conservative 32; Mismatches 60; Indels 0; Gaps 0;
 Qy 1 MKRQNYRTLALIYCTTYLVAAYVDALESEPELTERORLELROELRARNLNSGGYE 60
 Db 1 MRRPSVRAAGLVLCTLYLVAAYVDALESEPELTERORLELROELRARNLNSGGYE 60
 Qy 61 ELERVVLRLKHKAGQWRFAGSFYAITVITIGHAAFTSTGGKVFCMFYALIGIPL 120
 Db 61 ELERLALQAEPRHAGROWKFGPSFYAITVITIGHAAFTSTGGKVFCMFYALIGIPL 120
 Qy 121 TLYMFOSLGERINTLVYLHRAKKGIGMRRADVSAMMVNLIGFFCISTICIGAAFSH 180
 Db 121 TLVTFOSLGERLNAVVRLLIAAKCCLGLRVCSTENLVAAGLCAATLALGAVAFSH 180
 Qy 181 YEHWTFFQAYYCFTLTIGFGDYVALQKDALQTOPQYVAFSFVYILGLTIGAFLN 240
 Db 181 FEGWTFPHAYYCFTLTIGFGDYVALQKDALQTOPQYVAFSFVYILGLTIGAFLN 240
 Qy 241 LVVLREMTMNAEDEKRA 258
 Db 241 LVVLRELVASADWPERAA 258

RESULT 12
 US-09-864-761-4389
 ; Sequence 34389, Application US/09864761
 ; Patent No. US2002004873A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharron G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanel, David K.
 ; APPLICANT: Chen, Wensheng
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 ; FILE REFERENCE: Acomica-X-1
 ; CURRENT APPLICATION NUMBER: US/09/864,761
 ; CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312
 PRIOR FILING DATE: 2000-02-04
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: US 09/632,366
 PRIOR FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: GB 24263,6
 PRIOR FILING DATE: 2000-10-04
 PRIOR APPLICATION NUMBER: US 60/236,359
 PRIOR APPLICATION NUMBER: PCT/US01/00666
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00667
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00664
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00669
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00665
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00668
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00670
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: US 60/234,687
 PRIOR FILING DATE: 2000-09-21
 PRIOR APPLICATION NUMBER: US 09/608,408
 PRIOR FILING DATE: 2000-06-30
 PRIOR FILING DATE: 2001-01-29
 NUMBER OF SEQ ID NOS: 49117
 SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
 SEQ ID NO 34389
 LENGTH: 279
 ;
 ORGANISM: Homo sapiens
 TYPE: PRT
 FEATURE: ;
 OTHER INFORMATION: Lazdunski, Michel
 FEATURE: MAP TO AC007859.1
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.8
 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.2
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.2
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5
 OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 5.2
 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.8
 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.3
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.1
 OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 4.3
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 5.5
 OTHER INFORMATION: EXPRESSED IN ES1-HUMAN HIT: BE378534.1, EVALUE 4.00e-43
 OTHER INFORMATION: SWISSPROT HIT: P34410, EVALUE 2.00e-11
 ;
 US-09-864-761-34389
 Query Match 37.9%; Score 774; DB 10; Length 370;
 Best Local Similarity 56.3%; Pred. No. 3..3e-64; Matches 169; Conservative 27; Mismatches 82; Indels 22; Gaps 5;
 Qy 96 YGHAAPSTDGKVKFCMFYALIGIPLTUVMFOSLGERINTLVRLHRAKKGLGMRADVS 155
 Db 1 YGHRAPGTDAGKAFKCMFYAVLGLPILTMFOSLGERINTLVRLKRIKCGMRADVS 60
 Qy 156 MAMVLIGFSCISTCIGAAFSHYEWTFRQAYVCFITLIGFQDVALQDKDQL 215
 Db 61 MENNVTGFFSGCNGTICGAAFSQOEWSSFHAYXCFITLIGFQDVALQDKGALQ 120
 Qy 216 TOPOYVARSFVYLTGTVIGAFLNVLVLFMMADEKRD-AEHRALLTRN 275
 Db 121 KPKLVAFSPMFYILVGLVIGAFLNVLVLFMMADEKRD-AEHRALLTRN-----AGNR 174
 ;
 RESULT 13
 US-09-939-484-8
 ; Sequence 8, Application US/09939484
 ; Patent No. US200203322A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Duprat, Fabrice
 ; APPLICANT: Leage, Florian
 ; APPLICANT: Flink, Michel
 ; APPLICANT: Lazdunski, Michel
 ; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
 ; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
 ; FILE REFERENCE: 1201-CIP-DIV-00
 ; CURRENT APPLICATION NUMBER: US/09/939,484
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: 09/144,914
 ; PRIOR FILING DATE: 1998-09-01
 ; PRIOR APPLICATION NUMBER: 08/749,816
 ; PRIOR FILING DATE: 1996-11-15
 ; PRIOR APPLICATION NUMBER: 60/095,234
 ; PRIOR FILING DATE: 1998-08-04
 ; PRIOR APPLICATION NUMBER: FR 96/01565
 ; PRIOR FILING DATE: 1995-02-08
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 8
 ; LENGTH: 370
 ; TYPE: PRT
 ; ORGANISM: Murine
 ; FEATURE: ;
 ; OTHER INFORMATION: TREK-1
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 US-09-939-484-8
 Query Match 18.1%; Score 370; DB 10; Length 370;
 Best Local Similarity 31.6%; Pred. No. 2.5e-26; Matches 93; Conservative 57; Mismatches 102; Indels 42; Gaps 9;
 Matches 93; Conservative 57; Mismatches 102; Indels 42; Gaps 9;
 Qy 1 MKRQNVRNTALIVTYCTFTYLGVAAWDALESEPELERORLERQOELRARYNLSQGYE 60
 Db 42 MKWKTIVSTIFLVV--VLYLIGAVKALEQPOBISQRTIVIQQTIAHQACVS--T 97
 Qy 61 ELERVVLRL-KPHKGV-----QWRFAGSFYAITVITIGYHAAPSTDGKV 108
 Db 98 ELDLIIQOIVAAATNAGIIPLGNNSNQVSHWDGSSFFAGFTVITIGRGNISPRTEGK 157
 Qy 109 FCMEYALIGIPLTUVMFOSLGERINTLVRLHRAKKGLGMRAD-----VSM 156
 Db 158 FCIIYALIGIPLGIPLEGGFLAGVGQDQLTIF-----OKGIKVEDEPIKWNQSQTKIRI 208
 Qy 157 ANMYLIGFSCISTCIGAAFSHYEWTFRQAYVCFITLIGFQDVALQDKDQLT 216
 Db 209 ISTIFILIGFCVILVALPAVIFKHEGMSALDAVYFVWVITLIGFQDVALQDKGALQ 266
 Qy 217 QPYVAFSPVYLTGTVIGAFLNVLVLFMMADEKRD-AEHRALLTRN 267
 Db 267 LDFYKPVVWFWLVLGVAYFAAVLMSIGDWLVRISKKUTEVEGFRHAEMTN 320
 ;
 RESULT 14
 US-09-939-483-8
 ; Sequence 8, Application US/09939483
 ; Patent No. US2002034558A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Duprat, Fabrice

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Copyright (c) 1993 - 2003
Gencore version
OM protein - protein search, using SW model
Run on: July 1, 2003, 15:11:12 ; Seq

(without alignments) 729.177 Million cell updates/sec

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Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen Parameters: 908470
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%

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database : R_Geneseq_101002:
1: /SIDS2/gcgdata/geneseq/
2: /SIDS2/gcgdata/geneseq/

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3 : /SIDS2/gcadata/geneseq/geneseq -emb1/AA1982.DAT:*
4 : /SIDS2/gcadata/geneseq/geneseq -emb1/AA1983.DAT:*
5 : /SIDS2/gcadata/geneseq/geneseq -emb1/AA1984.DAT:*
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8: /SIDS2/gcadata/geneseq/geneseq -emb1/AA1987.DAT:*
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10: /SIDS2/gcadata/geneseq/geneseq -emb1/AA1989.DAT:*
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17: /SIDS2/gcdata/geneseq/geneseq -emb1/A1196.DAT:*
18: /SIDS2/gcdata/geneseq/geneseq -emb1/A1197.DAT:*
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19: /SIDSS2/gcdata/geneseq/geneseq-embI/AA1998.DAT:*
20: /SIDSS2/gcdata/geneseq/geneseq-embI/AA1999.DAT:*
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21: /SID52/gcadata/geneseq/geneseq-p-emb1/AA2001.DAT: *
22: /SID52/gcadata/geneseq/geneseq-p-emb1/AA2002.DAT: *
23: /SID52/gcadata/geneseq/geneseq-p-emb1/AA2002.DAT: *
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Pred. No. 1 is the number of results predicted by chance to have a score greater than or equal to the score of the result being predicted.

and is derived by analysis of the total score distribution.

Result: **Query** **Summaries**

No.	Score	Match	Length	DB	ID	Description
1	2042	100.0	394	21	AAE10343	Murine tag

2	2042	100.0	394	RAY79674
3	2042	100.0	394	RAY87291
4	600	600	600	600

4	189.1	405	21	RAY95230
5	60.5	309	22	AAU96230
6	54.7	374	21	AAB18807
				.

7	1116	54.7	374	21	AAB18813	Protein er
8	1116	54.7	374	22	RAG63938	Amino acid
9	1116	54.7	374	23	AAE22991	Twink
10	1116	54.7	374	23	AAE13279	Human trin

SUMMARIES

ALIGNMENTS

XX
 PS Claim 23; Page 34-35; 39pp; English.
 XX
 CC the invention relates to human and mouse TREK-1 potassium channel
 CC proteins and their corresponding DNA molecules. TREK-1 nucleic acid is
 CC useful for transfecting cells to induce expression of the TREK-1
 CC potassium channel protein. These cells are then used in assays to
 CC identify compounds which have anaesthetic properties, producing a safe,
 CC reversible state of unconsciousness with concurrent amnesia and analgesia
 CC in a mammal upon inhalation. The present sequence is murine TASK
 XX potassium channel protein related to the invention.

Sequence 394 AA:

Query Match 100.0%; Score 2042; DB 21; Length 394;
 Best Local Similarity 100.0%; Pred. No. 7. 8e-214; Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 MKRNVRTALIVCTFTYLGVAAVDALESEPELIERORLERQOELRQARYNLSQLGYE 60
 Qy 61 ELERVVLRIKPHKAGVONRFAGSFYFAITWITVITIGHAAPSPDGKVKFCMVALGLP 120
 Db 61 ELERVVLRIKPHKAGVONRFAGSFYFAITWITVITIGHAAPSPDGKVKFCMVALGLP 120
 Qy 121 TLWMFQSLGERINTLVLRLHRAKKGGLGNRADSVMANVLGFFSCISTLCTGAAAFSH 180
 Db 121 TLWMFQSLGERINTLVLRLHRAKKGGLGNRADSVMANVLGFFSCISTLCTGAAAFSH 180
 Qy 181 YEHWTFQAVYCYCTLTIGFQYVALQDQALQTQPOYVAFVYVLTGLVIGAFLN 240
 Db 181 YEHWTFQAVYCYCTLTIGFQYVALQDQALQTQPOYVAFVYVLTGLVIGAFLN 240
 Qy 241 LVVLFMTNAEDEKRDRAHRLTRNQAGGGGGGSAHTDTASSPAAGGGGERFNVY 300
 Db 241 LVVLFMTNAEDEKRDRAHRLTRNQAGGGGGGSAHTDTASSPAAGGGGERFNVY 300
 Qy 301 AEVLHFQSMCSCLWYKSRBKLOQYSPIMIPRDLSSTDTCVEQSHSPGGGRYSDTPSRR 360
 Db 301 AEVLHFQSMCSCLWYKSRBKLOQYSPIMIPRDLSSTDTCVEQSHSPGGGRYSDTPSRR 360
 Qy 361 CICSGAPRASIASSVSTGLHSLSTFRGLAKR RSSV 394
 Db 361 CICSGAPRASIASSVSTGLHSLSTFRGLAKR RSSV 394

RESULT 2

AY79674 AY79674 standard; Protein; 394 AA.
 XX
 AC AY79674;
 XX
 DT 29-AUG-2000 (first entry)
 XX
 DE Human potassium channel TASK1.
 XX
 KW TASK1; TWIK-related acid-sensitive K⁺ channel 1; human;
 KW potassium channel; drug screening; hypertension;
 KW hypotensive; epilepsy; arrhythmia; vascular diseases;
 KW neurodegenerative disease; ischaemia; anoxia; endocrine disease;
 KW muscle disease; therapy.
 'XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 53 /note- "N-glycosylated"
 FT Modified-site 323 /note- "O-phosphorylated"
 FT Modified-site 383 /note- "O-phosphorylated"
 FT Modified-site 392 /note- "O-phosphorylated"

FT Modified-site /note- "O-phosphorylated"
 FT /note- "O-phosphorylated"
 FT WO200027871-A2.
 PN XX
 PD 18-MAY-2000.
 PR 09-NOV-1999; 99W0-1B01886.
 PR 09-NOV-1998; 98US-0107692.
 PR 08-NOV-1999; 99US-0436265.
 XX
 PA (CNRS) CNRS CENT NAT RECH SCI.
 XX
 PI Duprat, F., Lesage, F., Lazdunski, M.;
 XX
 DR WPI; 2000-316487/32.
 N-PDB: AAA27746.
 PT New nucleic acid encoding a non-inactivating outwardly rectifying
 PT potassium transport channel, designated TASK2, useful in the treatment
 PT of hypertension or dysfunctions of the kidney, liver or pancreas.
 XX
 PS Disclosure: Fig 8; 91pp; English.
 XX
 The present sequence is that of human TASK1 (TWIK-related
 CC acid-sensitive K⁺ channel), a member of a new family of 2p
 CC domain potassium channels, also including TWK-1 (see AA79673) and
 CC novel TASK2 (see AA79675). TASK1 is expressed in many different
 CC tissues, and at particularly high levels in pancreas and placenta.
 CC Host cells expressing TWK-1 family members can be used to screen
 CC for substances that modulate the activity of members of the TWK-1
 CC family of potassium channels. The drugs identified may be
 CC useful in the treatment of diseases of the heart or of the nervous
 CC system, such as epilepsy, arrhythmia, vascular diseases,
 CC neurodegenerative diseases, kidney, liver or pancreas diseases,
 CC hypertension, diseases associated with ischaemia or anoxia,
 CC endocrine diseases associated with anomalies of hormone secretion,
 CC and muscle diseases.
 XX
 Sequence 394 AA;

Query Match 100.0%; Score 2042; DB 21; Length 394;
 Best Local Similarity 100.0%; Pred. No. 7. 8e-214; Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 MKRNVRTALIVCTFTYLGVAAVDALESEPELIERORLERQOELRQARYNLSQLGYE 60
 Qy 61 ELERVVLRIKPHKAGVONRFAGSFYFAITWITVITIGHAAPSPDGKVKFCMVALGLP 120
 Db 61 ELERVVLRIKPHKAGVONRFAGSFYFAITWITVITIGHAAPSPDGKVKFCMVALGLP 120
 Qy 121 TLWMFQSLGERINTLVLRLHRAKKGGLGNRADSVMANVLGFFSCISTLCTGAAAFSH 180
 Db 121 TLWMFQSLGERINTLVLRLHRAKKGGLGNRADSVMANVLGFFSCISTLCTGAAAFSH 180
 Qy 181 YEHWTFQAVYCYCTLTIGFQYVALQDQALQTQPOYVAFVYVLTGLVIGAFLN 240
 Db 181 YEHWTFQAVYCYCTLTIGFQYVALQDQALQTQPOYVAFVYVLTGLVIGAFLN 240
 Qy 241 LVVLFMTNAEDEKRDRAHRLTRNQAGGGGGGSAHTDTASSPAAGGGGERFNVY 300
 Db 241 LVVLFMTNAEDEKRDRAHRLTRNQAGGGGGGSAHTDTASSPAAGGGGERFNVY 300
 Qy 301 AEVLHFQSMCSCLWYKSRBKLOQYSPIMIPRDLSSTDTCVEQSHSPGGGRYSDTPSRR 360
 Db 301 AEVLHFQSMCSCLWYKSRBKLOQYSPIMIPRDLSSTDTCVEQSHSPGGGRYSDTPSRR 360
 Qy 361 CICSGAPRASIASSVSTGLHSLSTFRGLAKR RSSV 394

RESULT 3	CC	antagonists, in competitive drug screens, and for purification of HSPP
AAV87291	CC	from natural sources.
AAV87291 standard; Protein; 394 AA.	XX	
AC	XX	
AAV87291;	XX	
DT 11-MAY-2000 (first entry)	XX	
XX	DE	Human signal peptide containing protein HSPP-68 SEQ ID NO:68.
XX	XX	Human: signal peptide-containing protein; HSPP; diagnosis; cancer; inflammation; cardiovascular disease; anticancer; anti-inflammatory; antimicrobial; nontropic; neuroprotective; cardiovascular; hepatotrophic; antiasthmatic; gene therapy; cell proliferation; neurological disorder; reproductive disorder; developmental disorder; arteriosclerosis; cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia; asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia; Parkinson's disease; Huntington's diseases; ovulatory defect; muscular dystrophy.
OS	OS	Homo sapiens.
XX	W020000610-A2.	
PN	XX	
PD 06-JAN-2000.	XX	
XX	PF 25-JUN-1999;	99WO-US1484.
XX	PR 26-JUN-1998;	98US-0090762.
PR 31-JUL-1998;	PR 01-OCT-1998;	98US-0094983.
PR 11-DEC-1998;	PR 98US-0112129.	
PA	PA	(INCY-) INCYTE PHARM INC.
XX	PAI P.	Lai P., Tang YT., Gorgone GA., Corley NC., Guegler KJ., Baughn MR;
PI	PI	Nkerblom IE., Au-Young J., Yue H., Patterson C., Reddy R., Hillman JL;
PI	XX	Bandman O;
DR	XX	WPI: 2000-160673/14.
N-PSDB; AAZ8176.	XX	
PT	PT	New human signal peptide-containing proteins useful in treatment, prevention and diagnosis of e.g. cancer, inflammation and cardiovascular disease.
PT	XX	Claim 1: Page 207-208; 327pp; English.
PS	XX	AAZ8109 to AAZ8242 encode AAV87224 to AAV87357 which represent the human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have antineoplastic, anti-inflammatory, antimicrobial, nontropic, hepatotropic, neuroprotective, cardiovascular and antiasthmatic activities, and can be used in gene therapy. HSPPs can be used to treat or prevent disorders associated with decreased activity or function of HSPP. Antagonists of HSPP are used to treat or prevent disorders associated with increased activity or function of HSPP. Such diseases include cell proliferation (including cancer), inflammation, cardiovascular, neurological, reproductive or developmental disorders, (e.g. arteriosclerosis, cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia, asthma, Crohn's disease, microbial or other infections, congestive or ischaemic heart disease, Alzheimer's, Parkinson's, Huntington's diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP nucleic acids can be used for the recombinant production of HSPP, for detecting HSPP in standard hybridisation and amplification assays (for diagnosis and monitoring), in gene therapy, as antisense, triplex-forming or ribozyme therapeutics, for detecting related sequences or genetic variations, and for chromosomal mapping. HSPP are also used to raise specific antibodies (Ab) and to screen for agonists and antagonists (potential therapeutic agents). Ab are used to diagnose, or monitor, HSPP-related diseases (in usual immunoassays), as therapeutic
RESULT 4	CC	
AAV95230	CC	
ID AAV95230 standard; Protein; 405 AA.	XX	
AC AAV95230;	XX	
DT 29-AUG-2000 (first entry)	XX	
DE Mouse potassium channel TASK.	XX	
PT TASK: TWIK-related acid-sensitive K ⁺ channel; mouse;	XX	
KW potassium channel; drug screening; hypertension;	XX	
KW hypotensive; epilepsy; arrhythmia; vascular diseases; neurodegenerative disease; ischaemia; anoxia; endocrine disease; muscle disease; therapy.	XX	
OS	OS	Mus musculus.
XX	XX	
Key	FH	Location/Qualifiers
Modified-site	FH	5.0
FT	FT	/note- "N-glycosylated"
FT	FT	334
Modified-site	FT	/note- "O-phosphorylated"
FT	FT	403
Modified-site	FT	/note- "O-phosphorylated"
FT	FT	404
Modified-site	FT	/note- "O-phosphorylated"
XX	PN	W0200027871-A2.
XX	PD	18-MAY-2000.
XX	PR	09-NOV-1998; 99WO-1B01886.
XX	PR	09-NOV-1998; 98US-0107692.

PR 08-NOV-1999; 990S-0436265.
 XX
 PA (CNRS) CNRS CENT NAT RECH SCI.
 XX
 PI Duprat F, Lesage F, Lazdunski M;
 XX
 DR WPI: 2000-376487/32.
 XX
 PT New nucleic acid encoding a non-inactivating outwardly rectifying potassium transport channel, designated TASK2, useful in the treatment of hypertension or dysfunctions of the kidney, liver or pancreas
 XX
 PS Disclosure: Fig 8; 91pp; English.
 XX
 CC The present sequence is that of murine TASK (TWIK-related acid-sensitive K⁺ channel), also including human TWIK-1 (see AAX79675), human TASK1 (see AAY9674) and novel human TASK2 (see AAY79675). Human and mouse TASK proteins share 85% identity, indicating that they are products of orthologue genes. Host cells expressing TWIK-1 family members can be used to screen for substances that modulate the activity of members of the TWIK-1 family of potassium channels. The drugs identified may be useful in the treatment of diseases of the heart or of the nervous system, such as epilepsy, arrhythmia, vascular diseases, neurodegenerative diseases, kidney, liver or pancreas diseases, hypertension, diseases associated with ischaemia or anoxia, endocrine diseases, associated with anomalies of hormone secretion, XX
 CC and muscle diseases.
 XX
 Sequence 405 AA:
 Query Match 89.1%; Score 1819; DB 21; Length 405;
 Best Local Similarity 88.1%; Pred. No. 1.8e-18; Matches 357; Conservative 9; Mismatches 25; Indels 14; Gaps 2;
 CC
 OY 4 QNVRTLALIVCTFVLLVGAVALDALESPPELTERQRLERQELRARNLNSGGYEELE 63
 DB 1 ENVRTLALIVCTFVLLVGAVALDALESPPEMTERQRLERQELRARNLNSGGYEELE 60
 CC
 OY 64 RVVRLKPKHAGYOWRFAAGSFYFAITVTTGIGHAAPSTGSKVFCMAYALIGIPLTV 123
 DB 61 RVVRLKPKHAGYOWRFAAGSFYFAITVTTGIGHAAPSTGSKVFCMAYALIGIPLTV 120
 CC
 OY 124 MFQSLGERINTSYRLHRAKKGLGMRADVSMAANVILGFFSCISTICIGAAFSYEEH 183
 DB 121 MFQSLGERINTSYRLHRAKKGLGMRADVSMAANVILGFFSCISTICIGAAFSYEEH 180
 CC
 OY 184 WTEFOQAYYCFITLTIGFQDVALQKQDQALQTOPQVAFYVILGIGFLNIV 243
 DB 181 WTEFOQAYYCFITLTIGFQDVALQKQDQALQTOPQVAFYVILGIGFLNIV 240
 CC
 OY 244 LREMTMNADEKRDAAHRLTRNGQAGGGG-----GGSAAHTDTASSTAA---- 291
 DB 241 LREMTMNADEKRDAAHRLTRNGQAGGGG-----GGSAAHTDTASSTAA---- 290
 CC
 OY 292 -GGGGFRNYYAEVLFHOMCSCLUWYKREKLOQYIPIPROLSTSPOVCFSHSSPGG 349
 DB 301 GVGCGSGFRNYYAEVLFHOMCSCLUWYKREKLOQYIPIPROLSTSPOVCFSHSSPGG 360
 CC
 OY 350 GGRYSDTSSRCCLSGARSATSVSTGLSLSFRGLMKRSSV 394
 DB 361 GGRYSDTSSRCCLSGARSATSVSTGLSLSFRGLMKRSSV 405
 RESULT 5
 AAU07620 ID AAU07620 standard; Protein: 309 AA.
 XX
 AC AAU07620;
 XX
 DT 21-NOV-2001 (first entry)
 XX
 DE Mouse 2P channel protein #1.
 XX
 KW Transmembrane potassium ion channel protein; inward potassium flux; pest control; membrane potential; pesticide; antihelmintic; nematode; insect; 2P channel; mouse.
 XX
 OS Mus musculus.
 XX
 PN WO2001006-A2.
 XX
 PR 15-FEB-2000; 20000S-0503849.
 XX
 PD 23-AUG-2001.
 XX
 PI 14-FEB-2001; 2001WO-US04680.
 XX
 DR WPI: 2001-536570/59.
 XX
 DR N-PSDB; AAS12179.
 XX
 PT New polypeptide, a mutant potassium ion channel protein for improving inward potassium flux under acidic conditions
 XX
 PS Example 18; Page 53; 131pp; English.
 XX
 CC The invention relates to a mutant potassium ion channel protein, having four membrane spanning domains and two pore forming domains, comprising a mutation at the second pore forming domain. The expression of the mutant protein in a cell confers improved inward potassium flux and the ability to grow in the presence of potassium. Mutant proteins and their corresponding polynucleotide sequences can therefore be used to improve inward potassium flux into cells under acidic conditions by modulating the membrane potential using therapeutic agents. The sequences may be used to develop agonists and antagonists of potassium channel proteins in order to control pests such as nematodes and insects. This sequence represents a mouse 2P channel protein:
 XX
 Sequence 309 AA:
 Query Match 60.5%; Score 1235.5; DB 22; Length 309;
 Best Local Similarity 83.9%; Pred. No. 5.9e-126; Matches 250; Conservative 8; Mismatches 27; Indels 13; Gaps 3;
 CC
 OY 4 QNVRTLALIVCTFVLLVGAVALDALESPPELTERQRLERQELRARNLNSGGYEELE 63
 DB 13 ENVRTLALIVCTFVLLVGAVALDALESPPEMTERQRLERQELRARNLNSGGYEELE 72
 CC
 OY 64 RVVRLKPKHAGYOWRFAAGSFYFAITVTTGIGHAAPSTGSKVFCMAYALIGIPLTV 123
 DB 73 RVVRLKPKHAGYOWRFAAGSFYFAITVTTGIGHAAPSTGSKVFCMAYALIGIPLTV 132
 CC
 OY 124 MFQSLGERINTSYRLHRAKKGLGMRADVSMAANVILGFFSCISTICIGAAFSYEEH 183
 DB 133 MFQSLGERINTSYRLHRAKKGLGMRADVSMAANVILGFFSCISTICIGAAFSYEEH 192
 CC
 OY 184 WTEFOQAYYCFITLTIGFQDVALQKQDQALQTOPQVAFYVILGIGFLNIV 241
 DB 193 WTEFOQAYYCFITLTIGFQDVALQKQDQALQTOPQVAFYVILGIGFLNIV 249
 CC
 OY 242 WVLRFMTMNADEKRDAAHRLTRNGQAGGGG-----GGSAAHTDTASSTAA 291
 DB 250 WVLRFMTMNADEKRDAAHRLTRNGQAGGGLGSLSLGSGLGDRVRRPDTCAAAA 307
 RESULT 6
 AAB1807 ID AAB1807 standard; Protein: 374 AA.
 XX
 AC AAB1807;
 XX
 DT AAB1807;
 XX

DE	22-JAN-2001 (first entry)	Db	287 KADVPDLQSVCSCTYRSQD--YGRSVARQNSAKLAPPYHFSISYKIEEISPLK 343
XX	Amino acid sequence of a human DKCNI polypeptide.	Qy	360 RCLCGAPRSAISSVSTGLHSLSITFRGLMRKRSV 394
DE	Human; DKCNI; potassium channel; cancer; pulmonary disease; depression; cardiovascular disease; inflammatory disease; renal disease; pain; psychiatric disorder; schizophrenia; neurodegenerative disease; Alzheimer's disease; neurological disorder; migraine; epilepsy; sleep-related disorder; erectile dysfunction; alopecia.	Db	344 NSLFP---SPISSPGLHSFTDHORMKRRKV 374
KW	XX	RESULT 7	
KW	XX	ID AAB18813	
KW	OS Homo sapiens.	ID	AAB18813 standard; Protein; 374 AA.
XX	PN WO20053628-A2.	AC	AAB18813;
XX	DR	XX	XX
XX	PD 14-SEP-2000.	XX	DE Protein encoded by an EST related to a human DKCNI cDNA.
XX	PF 02-MAR-2000; 2000WO-EP01750.	XX	KW Human; DKCNI; potassium channel; cancer; pulmonary disease; depression; cardiovascular disease; inflammatory disease; renal disease; pain; psychiatric disorder; schizophrenia; neurodegenerative disease; Alzheimer's disease; neurological disorder; migraine; epilepsy; sleep-related disorder; erectile dysfunction; alopecia; expressed sequence tag; EST.
PR	05-MAR-1999; 99GB-0005061.	XX	KW
PR	10-FEB-2000; 2000GB-0003112.	XX	KW
PA	(SMIK) SMITHKLINE BEECHAM PLC.	XX	KW
XX	PI Duckworth DM, Godden RJ, Chapman CG, Meadows RJ;	XX	KW
XX	DR WPI; 2000-587424/55.	OS	KW
XX	N-PSDB; AAA75886.	XX	OS
PT	Polypeptides and polynucleotides of the potassium channel family, useful for identifying agonists/antagonists of therapeutic use and diagnosis and treatment of cancer, pulmonary, cardiovascular, inflammatory and renal disease -	XX	XX
PT	Claim 1; Page 25; 36pp; English.	XX	DE
XX	CC The present sequence represents human DKCNI polypeptide. The polypeptide is a member of the potassium channel family. The DKCNI polypeptides and polynucleotides are useful for treating diseases including cancer, pulmonary, cardiovascular, inflammatory or renal diseases, pain, psychiatric disorders including depression and schizophrenia, neurodegenerative disease including Alzheimer's, neurological disorders, migraine, epilepsy, sleep-related disorders, erectile dysfunction and alopecia. DKCNI polynucleotides are useful as diagnostic reagents for detecting mutations in the associated gene.	XX	KW
CC	XX	XX	KW
CC	Sequence 374 AA;	XX	OS
PS	Query Match 54.7%; Score 1116; DB 21; Length 374; Best Local Similarity 59.0%; Pred. No. 8.7e-113; Matches 233; Conservative 44; Mismatches 96; Indels 22; Gaps 5;	XX	XX
Qy	1 MKRQNVRTLALIVCTFTYLVGAFFDALESEPELIERORLERLRLQELRARNYNSQGGE 60	XX	XX
Db	1 MKRQNVRTLALIVCTFTYLVGAFFDALESEPELIERORLERLRLQELRARNYNSQGGE 60	XX	CC
Qy	61 ELEVRVLRKPKHAGVQWRFAGSFYFAITVITITGHAAPSTGKVCFMFYALIGPL 120	XX	CC
Db	61 QLELVILQSEPHRAGVQWRFAGSFYFAITVITITGHAAPSTGKVCFMFYALIGPL 120	XX	CC
Qy	121 TLYMFQSGERINTLVRLHRAKKGHLRRADYSMANVNLIGFESCLSTLCIGAAATSH 180	XX	CC
Db	121 TLYMFQSGERINTLVRLHRAKKGHLRRADYSMANVNLIGFESCLSTLCIGAAATSH 180	XX	CC
Qy	181 YERHTFFQAYYCFITLITGFGDVALQDKQALQTQPOVAVSFVYIITGLTVIGAFLN 240	XX	CC
Db	181 CEWMSFPHAYYCFITLITGFGDVALQDKQALQTQPOVAVSFVYIITGLTVIGAFLN 240	XX	CC
Qy	241 LIVVRLRFTMNAEDERDERRAHLRALTNGQAGGGGGSAITDPAASSTAAGGGFRNTY 300	XX	CC
Db	241 LIVVRLRFTMNAEDERDERRAHLRALTNGQAGGGGGSAITDPAASSTAAGGGFRNTY 300	XX	CC
Qy	241 LIVVRLRFTMNAEDERDERRAHLRALTNGQAGGGGGSAITDPAASSTAAGGGFRNTY 300	XX	CC
Db	241 LIVVRLRFTMNAEDERDERRAHLRALTNGQAGGGGGSAITDPAASSTAAGGGFRNTY 300	XX	CC
Qy	301 -AEVLHFDSMCSCLWYKSKPLQISIPMIPDLSSTDTCVEGSHSSCGGGYSDTPSP 359	XX	CC
Qy	1 MKRQNVRTLALIVCTFTYLVGAFFDALESEPELIERORLERLRLQELRARNYNSQGGE 60	Db	61 ELEVRVLRKPKHAGVQWRFAGSFYFAITVITITGHAAPSTGKVCFMFYALIGPL 120
Db	61 QLELVILQSEPHRAGVQWRFAGSFYFAITVITITGHAAPSTGKVCFMFYALIGPL 120	Db	61 QLELVILQSEPHRAGVQWRFAGSFYFAITVITITGHAAPSTGKVCFMFYALIGPL 120

CC as epilepsy, Alzheimer's disease, Parkinson's disease, stroke, multiple
 CC scleroposis, migraine), psychiatric disorders (such as depression, CC
 CC schizophrenia, bipolar disorders) and diseases related to heart
 CC (such as arrhythmias), diseases related to pancreas (such as
 CC pancreatitis and diabetes).

QY 121 TLVMEQSLGERINTLVRLHRAKKGLGRADYSMANNVLGFSCSTLCTGAATSH 180
 ||||| ||||| ||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 181 CEWSFFHAYYCITLTIGFQYVAKQDQALQTOPYVAFSFWYLTGLVIGATN 240
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 181 CEWSFFHAYYCITLTIGFQYVAKQDQALQTOPYVAFSFWYLTGLVIGATN 240
 Db 121 TLVMEQSLGERINTLVRLHRAKKGLGRADYSMANNVLGFSCSTLCTGAATSH 180
 ||||| ||||| ||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 181 CEWSFFHAYYCITLTIGFQYVAKQDQALQTOPYVAFSFWYLTGLVIGATN 240
 QY 241 LVVLFMTNAEDEKDAEHRALITRNGOAGGGGGSAHTTASSTAAGGGFRWY 300
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 241 LVVLFMTNAEDEKDAEHRALITRNGOAGGGGGSAHTTASSTAAGGGFRWY 300
 Db 241 LVVLFMTNAEDEKDAEHRALITRNGOAGGGGGSAHTTASSTAAGGGFRWY 300
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 241 LVVLFMTNAEDEKDAEHRALITRNGOAGGGGGSAHTTASSTAAGGGFRWY 300
 QY 287 KADYPPDLSQVSCCCTYRSQD--YGRSRVAPQNSFAKALPHYFHSISKIEISPILK 343
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 287 KADYPPDLSQVSCCCTYRSQD--YGRSRVAPQNSFAKALPHYFHSISKIEISPILK 343
 QY 360 RCLCGSAPRSAISSVSTGHLHSLSTFRGLKMRSSV 394
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 360 RCLCGSAPRSAISSVSTGHLHSLSTFRGLKMRSSV 394
 Db 344 NSLFP---SPISSISPGHLHSFTDHQRLMKRRKV 374
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 344 NSLFP---SPISSISPGHLHSFTDHQRLMKRRKV 374

RESULT 8

ID AAG63938

AA standard; Protein; 374 AA.

AC AAG63938;

XX

DT 29-OCT-2001 (first entry)

DE Amino acid sequence of human potassium channel protein KCNB.

XX

KW Human; potassium channel protein; KCNB; breast tissue; cancer; stroke; potassium channel-associated disorder; brain associated disorder; epilepsy; Alzheimer's disease; Parkinson's disease; multiple sclerosis; migraine; psychiatric disorder; depression; schizophrenia; diabetes; bipolar disease; heart disease; arrhythmia; pancreas disease; pancreatitis.

XX

OS Homo sapiens.

XX

PN WO20016741-A2.

XX

PD 13-SEP-2001.

XX

PP 02-MAR-2001; 2001WO-US06801.

XX

PR 03-MAR-2000; 2000US-0186915.

XX

PA (TULA-) TULARIK INC.

XX

PI Mu D, Powers S;

XX

WPI: 2001-522949-57.

DR N-PSDB; AAH74999.

XX

A nucleic acid encoding a potassium channel, termed KCNB (potassium channel expressed in breast), useful in the diagnosis, prognosis or treatment of diseases associated with altered KCNB activity or expression, e.g. cancer and diabetes -

XX

PS Claim 16; Page 79; 82pp; English.

XX

CC The present sequence represents a human potassium channel protein, termed KCNB. KCNB is expressed in breast tissue. The KCNB polypeptides are useful for identifying a compound that modulates its activity. The KCNB polypeptide and nucleic acid are useful for detecting cancer cells in biological samples. The inhibitor of the potassium channel polypeptide is useful for inhibiting proliferation of a cancer cell and for treating a potassium channel-associated disorder. The KCNB nucleic acids, proteins, and/or antibodies are useful in the diagnosis or prognosis, or treatment of diseases associated with altered KCNB activity or expression. Such diseases are cancer, brain associated disorders (such

CC

QY 121 TLVMEQSLGERINTLVRLHRAKKGLGRADYSMANNVLGFSCSTLCTGAATSH 180
 ||||| ||||| ||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 181 CEWSFFHAYYCITLTIGFQYVAKQDQALQTOPYVAFSFWYLTGLVIGATN 240
 Db 121 TLVMEQSLGERINTLVRLHRAKKGLGRADYSMANNVLGFSCSTLCTGAATSH 180
 ||||| ||||| ||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 181 CEWSFFHAYYCITLTIGFQYVAKQDQALQTOPYVAFSFWYLTGLVIGATN 240
 QY 241 LVVLFMTNAEDEKDAEHRALITRNGOAGGGGGSAHTTASSTAAGGGFRWY 300
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 241 LVVLFMTNAEDEKDAEHRALITRNGOAGGGGGSAHTTASSTAAGGGFRWY 300
 Db 241 LVVLFMTNAEDEKDAEHRALITRNGOAGGGGGSAHTTASSTAAGGGFRWY 300
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 241 LVVLFMTNAEDEKDAEHRALITRNGOAGGGGGSAHTTASSTAAGGGFRWY 300
 QY 287 KADYPPDLSQVSCCCTYRSQD--YGRSRVAPQNSFAKALPHYFHSISKIEISPILK 343
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 287 KADYPPDLSQVSCCCTYRSQD--YGRSRVAPQNSFAKALPHYFHSISKIEISPILK 343
 QY 360 RCLCGSAPRSAISSVSTGHLHSLSTFRGLKMRSSV 394
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 360 RCLCGSAPRSAISSVSTGHLHSLSTFRGLKMRSSV 394
 Db 344 NSLFP---SPISSISPGHLHSFTDHQRLMKRRKV 374
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 344 NSLFP---SPISSISPGHLHSFTDHQRLMKRRKV 374

RESULT 9

ID AAE22989

AAE22989 standard; Protein; 374 AA.

AC AAE22989;

XX

DT 21-AUG-2002 (first entry)

DE Human TWIK-9 protein.

XX

KW Human; tandem of P domains in a weak inward rectifying potassium channel; TWIK-9; 56115 protein; central nervous system disorder; sleep disorder; Alzheimer's disease; Parkinson's disease; autonomic function disorder; Huntington's disease; hypertension; neurosychiatric disorder; depression; schizophrenia; bipolar affective disorder; cardiac-related disorder; learning disorder; cellular proliferation disorder; migration disorder; myocardial infarction; memory disorder; arteriosclerosis; gene therapy; amnesia; pain disorder; cancer; prophylaxis.

XX

OS Homo sapiens.

XX

Key Location/Qualifiers

PH 1..24

FT Peptide /Label= Signal_peptide

FT Protein 25..374

FT Domain /note= "Mature human TWIK-9 protein"

FT /note= "Transmembrane domain 1"

FT Modified-site 31..34

FT /note= "Casein kinase II phosphorylation site"

FT Modified-site 53..56

FT /note= "N-glycosylation site"

XX 18-OCT-2001.
 XX PD
 XX 06-APR-2001; 2001WO-US11206.
 XX PR 06-APR-2000; 2000US-195595P.
 PR 12-APR-2000; 2000US-19872P.
 PR 20-APR-2000; 2000US-199020P.
 PR 28-APR-2000; 2000US-20052P.
 PR 05-MAY-2000; 2000US-20348P.
 PR 11-MAY-2000; 2000US-203495P.
 XX PA (INCY-) INCYTE GENOMICS INC.
 XX PI Reddy R, Thornton M, Borowsky ML, Tang YT, Khan FA, Tribouley CM;
 PI Gandhi AR, Yao MG, Sanjanwala MS, Baughn MR, Nguyen DB;
 PI Policky JL, Yue H, Seilhamer JJ, Walla NK, Lal P, Kearney L;
 PI Walsh RT, Lu DAM, Lu Y, Greene BD, Raumann BE, Patterson C;
 XX DR WPI; 2002-017448/02.
 DR N-PSDB; AAD21998.
 XX PT Polypeptides of human transporters and ion channels, useful for
 PT diagnosing, treating or preventing disorders of transport;
 PT neurological, muscle, immunological and cell proliferative disorders -
 PS XX
 Claim 1: Page 124-125; 150pp; English.
 The invention relates to human transporters and ion channels (TRICH) and the polynucleotides encoding them. The composition comprising TRICH or agonist of TRICH is useful for treating a disease or condition associated with decreased expression of functional TRICH or condition associated with overexpression of TRICH respectively. The composition comprising Ab is useful for diagnosing a condition of disease associated with expression of TRICH in a subject, where the disorders include a transport disorder such as akinesthesia, cystic fibrosis, diabetes mellitus, Parkinson's disease, myasthenia gravis, cardiac disorders associated with transport e.g. angina, hypertension, myocarditis, neurological disorders associated with transport e.g. Alzheimer's disease, Wilson's disease, schizophrenia, cataracts, Infective, hyperglycaemia, Gravé's disease, goitre, addison's disease, Huntington's disease, dementia, multiple sclerosis, bacterial and viral meningitis. TRICH DNA is useful for generating a transcript image of a tissue or cell type, which represents the global pattern of gene expression by a particular tissue or cell type and for analysing the proteome of a tissue or cell type. TRICH DNA is used in gene therapy. The present amino acid sequence is
 CC XX
 Sequence 374 AA;
 SQ Query Match 54.7%; Score 1116; DB 23; Length 374;
 Best Local Similarity 59.0%; Pred. No. 8; e-113; Matches 233; Conservative 44; Mismatches 96; Indels 22; Gaps 5;
 Oy 1 MKRQNRVTRALIVCFTFLVGAQVDALESEEEELIERQLEIRQELRQARYMISQCGYE 60
 Db 1 MKRQNRVTRILSLIVCTFTLIVGAVFADLESDHEWREPEKKAAEIRIKKGKINNISSEDR 60
 Oy 61 ELERVVLRIKPKHAGVQHFRAGSFYFATITVITITIGYGAAPSDGGKVFCMFYALIGPL 120
 Db 61 QLELVILQSEPHRAGVQKFGASFYFAITITVITITIGYGAAPSDGGKVFCMFYAVLGPL 120
 Oy 121 TLWFMOSIGERINIVLVLHRRKKGGLMRRADYSMANNLIGFFSCISTCIGAAMASH 180
 Db 121 TLWFMOSIGERINIVLVLHRRKKGGLMRRADYSMANNLIGFFSCISTCIGAAMASH 180
 Oy 181 YERHTFFQYVYCPITLMTGFSQYVALQDQALQTOPOYVAFSFWVITLIGLIGVIGFLN 240
 Db 181 CEEMSSFFHAYYCFITLTIGFQDVALQTKGALQKPLIVAFSFMILVGLIGVIGFLN 240
 Oy 241 LIVLRLFIMMNSDEERRDAEERASL-----AGNRNSMVTHIPEPRPS-----RPRY 300
 Db 241 LIVLRLFIMMNSDEERRDAEERASL-----AGNRNSMVTHIPEPRPS-----RPRY 286

RESULT 11
 ID AAEI0679
 ID AAEI0679 standard; Protein; 400 AA.
 AC AAEI0679;
 XX 18-DEC-2001 (first entry)
 XX DE Human TWIK-6 (G 165) protein.
 XX Human; Tandem of P domains in a weak Inward rectifying K⁺ channel-6;
 KW TWIK-6; sensory nervous system disorder; cardiac; cellular proliferation;
 KW hematopoietic; cytosolic; nootropic; osteopathic; gene therapy; mania;
 KW vaccine; potassium channel-associated disorder; Parkinson's disease;
 KW Alzheimer's disease; dementia; Huntington's disease; multiple sclerosis;
 KW anoxotropic; lateral sclerosis; hypertension; depression; inflammation;
 KW anxiety; amnesia; neuropsychiatric disorder; migraine; obesity; cancer;
 KW arteriosclerosis; ischaemia; cardiomyopathy; myocardial infarction;
 KW ataxia; arrhythmia; paroxysm; muscle weakness; cellular growth; tumour;
 KW carcinoma; leukaemia; hepatic disorder; gene therapy.
 XX OS Homo sapiens.
 XX FH
 FT Key location/Qualifiers
 FT Domain 75..144 /note= "TWIK-related ion channel domain"
 FT Domain 78..96 /label= "Transmembrane_domain"
 FT Domain 81..312 /note= "Potassium channel protein domain"
 FT Domain 150..166 /note= "P-loop_domain"
 FT Domain 178..195 /note= "Pore-loop domain"
 FT Misc-difference 165 /note= "Wild type Glu is substituted with Gly"
 FT Domain 229..248 /label= "Transmembrane_domain"
 FT Domain /label= "Transmembrane_domain"
 FT Domain 260..278 /label= "P-loop_domain"
 FT Domain /note= "Pore-loop domain"
 FT Domain 290..314 /label= "Transmembrane_domain"
 XX WO200166743-A2.
 XX PD 13-SEP-2001.
 XX P2-MAR-2001; 2001WO-US06933.
 PR 03-MAR-2000; 2000US-0518866.
 XX PA (MILL-) MILLENIUM PHARM INC.
 XX PI Curtiss RAJ, Glucksmann MA;
 XX DR WPI; 2001-596835-67.
 DR N-PSDB; AAD17526.
 XX PT Novel TWIK-5 polypeptide of TWIK family of potassium channels for
 PT treating sensory nervous system disorders, cardiac-related disorders
 PT and cellular proliferation disorders comprises the modulation of its

CC a food supplement; (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AB00010-ABG30177 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp://wipo.int/pub/published_pat_sequences.

XX Sequence 436 AA;

Query Match 38.5% Score 785.5: DB 22; Length 436;
 Best Local Similarity 51.1%; Pred. No. 1.3e-76; NMatches 179; NMatches 32; Mismatches 94; Indels 45; Gaps 8;
 Qy 54 LSQGGYEEELERVVRLPKPKHQVQWRFFAGGSFFAIIVVITI-----GYGAAPSTDG 105
 Db 123 LEAGGYG-----LNCAPNRSHLE-----ALTSNVTPEGDAFRRGGYGAAPGDA 167
 Qy 106 GKIFCMFYALLGIPPLTVLWFMQSIGERINTVLRVLLHRAKKGIGLGMRRADVSMMANVLGF 165
 Db 168 GKAFCMFYAVLGLPPLTMFQSIGERINTVVRLLKRIKKGICMRNTDVSMENNTVGF 227
 Qy 166 SCISTLCIGAAFSHYEWTFQAYYYCFITLUTIGFDDYVALQDQALQTPOYVAFSE 225
 Db 228 SCMETLCIGGAAFSQCEWSFFRAYYCFITLUTIGFDDYVALQTKGALKQKPLYVAFSE 287
 Qy 226 VVITLGLTVIGAFNLVYLRFMMADEKDEKRDEHRAALLTRNQAGGGGSAHMTDA 285
 Db 288 MYLIVGLTVIGAFNLVYLRFMNSEDERDEEASL-----AGNRNSMVTHIPEEP 341
 Qy 286 SSTAAGGGGFRNAY-AEWLHFOSMCSCLLWYKSREKIQSYIMIIPROLISTSDTCVQSH 344
 Db 342 RPS-----RERYKADVPDQSVCSQTCYRSQD--YGGRSVAPQNSFSAKLPHYFH 390
 Qy 345 SSPGGGGRSYDTPSRRCLCSGAPRSATSSVSVGLHSLSTFRGLMKRSSV 394
 Db 391 SISYKIEISPSLTKNSLPE---SPISISSPGLHSTDHQRLMKRKSV 436

Search completed: July 1, 2003, 15:15:39
 Job time : 83 secs

Run on: July 1, 2003, 15:18:47 ; Search time 27 Seconds
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OM protein - protein search, using sw model

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued Patents_AA:*

- 1: /cgn2_6/podata/1/1aa/5A_COMB_pep:*
- 2: /cgn2_6/podata/1/1aa/5B_COMB_pep:*
- 3: /cgn2_6/podata/1/1aa/6A_COMB_pep:*
- 4: /cgn2_6/podata/1/1aa/6B_COMB_pep:*
- 5: /cgn2_6/podata/1/1aa/PCTRUS_COMB_pep:*
- 6: /cgn2_6/podata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters: 262574

Searched: 262574 seqs, 29422922 residues

Summary

Result No.	Score	Query	Match	Length	DB	ID	Description
1	2042	100.0	394	4	US-09-144-914-4		Sequence 4, Appl1
2	1819	89.1	405	4	US-09-144-914-5		Sequence 5, Appl1
3	370	18.1	370	4	US-09-144-914-8		Sequence 8, Appl1
4	369	18.1	411	4	US-09-336-080-6		Sequence 6, Appl1
5	363	17.8	411	4	US-09-336-080-2		Sequence 2, Appl1
6	329.5	16.1	393	4	US-09-336-63A-83		Sequence 83, Appl1
7	329.5	16.1	393	4	US-09-332-470-2		Sequence 2, Appl1
8	329.5	16.1	393	4	US-09-332-470-4		Sequence 2, Appl1
9	320.5	15.7	336	3	US-09-322-816-2		Sequence 3, Appl1
10	295.5	14.5	313	4	US-09-144-914-2		Sequence 2, Appl1
11	253	12.4	336	1	US-08-332-312-4		Sequence 81, Appl1
12	231.5	11.3	618	1	US-08-332-312-2		Sequence 4, Appl1
13	190.5	9.3	383	3	US-08-349-816-4		Sequence 2, Appl1
14	190.5	9.3	383	4	US-09-144-914-7		Sequence 4, Appl1
15	190.5	9.3	383	4	US-09-144-914-7		Sequence 2, Appl1
16	176.5	8.6	107	4	US-09-236-080-4		Sequence 4, Appl1
17	156	7.6	347	3	US-08-449-816-3		Sequence 3, Appl1
18	156	7.6	347	4	US-09-144-914-6		Sequence 6, Appl1
19	131.5	6.4	646	4	US-09-336-63A-10		Sequence 10, Appl1
20	113	5.5	197	4	US-09-336-643A-16		Sequence 16, Appl1
21	112.5	5.5	1082	4	US-09-336-63A-20		Sequence 20, Appl1
22	112.5	5.5	1083	4	US-09-500-776-2		Sequence 2, Appl1
23	111.5	5.5	1083	4	US-09-343-494-1		Sequence 1, Appl1
24	111.5	5.5	636	4	US-09-178-109-4		Sequence 2, Appl1
25	111.5	5.5	636	4	US-09-142-791A-2		Sequence 4, Appl1
26	111.5	5.5	655	4	US-09-142-791A-4		Sequence 2, Appl1
27	111.5	5.5	655	4	US-09-178-109-2		Sequence 2, Appl1

Summary

RESULT 1
 US-09-144-914-4

SEQUENCE 4, Application US/09144914

PATENT NO. 630955

GENERAL INFORMATION:

APPLICANT: Duprat, Fabrice

APPLICANT: Lesage, Florian

APPLICANT: Flink, Michel

APPLICANT: Lazardski, Michel

TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS

TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS

FILE REFERENCE: 989_6705CIP

CURRENT APPLICATION NUMBER: US/09/144,914

CURRENT FILING DATE: 1998-09-01

EARLIER APPLICATION NUMBER: 08/7749, 816

EARLIER FILING DATE: 1996-11-15

EARLIER APPLICATION NUMBER: 60/095,234

EARLIER FILING DATE: 1998-08-04

EARLIER APPLICATION NUMBER: FR 96/01565

EARLIER FILING DATE: 1996-02-08

NUMBER OF SEQ ID NOS: 24

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 4

LENGTH: 394

TYPE: PRT

ORGANISM: HOMO SAPIENS

FEATURE:

OTHER INFORMATION: TASK

US-09-144-914-4

Query Match 100.0%; Score 2042; DB 4; Length 394;

Best Local Similarity 100.0%; Pred. No 4.9e-218; Mismatches 0; Indels 0; Gaps 0;

Matches 394; Conservative 0; Pairs 0;

QY

1 M K R Q N V R T L A L I V C T F T Y L W G A A F D A L E S P E L E R O R E L Q D E L R A R Y N L S O G G Y E

1 M K R Q N V R T L A L I V C T F T Y L W G A A F D A L E S P E L E R O R E L Q D E L R A R Y N L S O G G Y E

Db

1 L V M F O S L G E R I N T Y V R Y L H R A K G L G M R A D V S A M V I G F S C I S T C I G A A F S H

1 E L E R V V L R K P H K A Q V O R P G S F A I T V T T G Y H A M P S T D G K V C F M Y A L G I P L

61 E L E R V V L R K P H K A Q V O R P G S F A I T V T T G Y H A M P S T D G K V C F M Y A L G I P L

61 E L E R V V L R K P H K A Q V O R P G S F A I T V T T G Y H A M P S T D G K V C F M Y A L G I P L

121 L V M F O S L G E R I N T Y V R Y L H R A K G L G M R A D V S A M V I G F S C I S T C I G A A F S H

121 L V M F O S L G E R I N T Y V R Y L H R A K G L G M R A D V S A M V I G F S C I S T C I G A A F S H

121 L V M F O S L G E R I N T Y V R Y L H R A K G L G M R A D V S A M V I G F S C I S T C I G A A F S H

121 L V M F O S L G E R I N T Y V R Y L H R A K G L G M R A D V S A M V I G F S C I S T C I G A A F S H

180 Y E H W T F F Q A Y Y C F T L T T G F G D Y V A L Q D A L O T O P O V A F S V W Y L Q G T V I G A F L N

180 Y E H W T F F Q A Y Y C F T L T T G F G D Y V A L Q D A L O T O P O V A F S V W Y L Q G T V I G A F L N

240 Y E H W T F F Q A Y Y C F T L T T G F G D Y V A L Q D A L O T O P O V A F S V W Y L Q G T V I G A F L N

240 Y E H W T F F Q A Y Y C F T L T T G F G D Y V A L Q D A L O T O P O V A F S V W Y L Q G T V I G A F L N

TYPE: PRT
 ORGANISM: Mus musculus
 US-09-236-080-6.

Query Match 18.1%; Score 369; DB 4; Length 411;
 Best Local Similarity 31.6%; Pred. No. 2, 4e-32; Indels 42; Gaps 9;
 Matches 93; Conservative 57; Mismatches 102; Length: 411

QY 1 MKRQNRNTRALIIVCTYLYGAAVDALESEPELERQERLROQELRARNLNSQGGYE 60
 Db 42 MKWKTGSTIFLVW-VLYLITGAAVFKALBQPOEISORTTIVIQKTFIQHACVNS-T 97
 QY 61 ELEVRVRL-KPHKAGV-----QWRFAGSFYFAITVITTYGHAAPSTDGKV 108
 Db 98 EDELIQOIVAAINAGIIPGNTSNQISHMDLGSSFFAGVITIGFGNISPRTEGGKI 157
 QY 109 FCMFYALGIGIPLTVLNFOSLGERINTLVRLHRAKKGHLRRAD-----VSM 156
 Db 158 FCIYIALLGIPLGFLLAGVGDQLGTF-----GKGIAKVETFIKWNVSQTKIRI 208
 QY 157 ANMLIGFFSCISTICIGAAFRSHYEWHTFOAQYVCFITLTIGFGDVALQKDOALQT 216
 Db 209 ISTIITILFGCVLFLVALPAIIFKHTBKGWSALDAIYFWVITLTIGFGDYYAGSD--IEV 266
 QY 217 QPYVVAFSFVYLITLGIVGAAFLNLY-VLRFMTMNAEDEKD-AEHRAALTRN 267
 Db 267 LDFYKPVVWFLVGLAYFAVLMSMGDWLRVSKTKKEEVGEFRRAAETAN 320

RESULT 5
 US-09-236-080-2
 ; Sequence 2, Application US/09236080
 ; GENERAL INFORMATION:
 ; APPLICANT: Helen Meadows
 ; TITLE OF INVENTION: No. 6242217el Compounds
 ; FILE REFERENCE: GP30031
 ; CURRENT APPLICATION NUMBER: US-09/236,080
 ; CURRENT FILING DATE: 1999-01-25
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 2
 ; LENGTH: 411
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-336-643A-83

Query Match 17.8%; Score 363; DB 4; Length 411;
 Best Local Similarity 31.0%; Pred. No. 1, 1e-31; Indels 42; Gaps 9;
 Matches 91; Conservative 59; Mismatches 102; Length: 411

QY 1 MKRQNRNTRALIIVCTYLYGAAVDALESEPELERQERLROQELRARNLNSQGGYE 60
 Db 42 MKWKTGSTIFLVW-VLYLITGAAVFKALBQPOEISORTTIVIQKTFIQHACVNS-T 97
 QY 61 ELEVRVRL-KPHKAGV-----QWRFAGSFYFAITVITTYGHAAPSTDGKV 108
 Db 98 EDELIQOIVAAINAGIIPGNTSNQISHMDLGSSFFAGVITIGFGNISPRTEGGKI 157
 QY 109 FCMFYALGIGIPLTVLNFOSLGERINTLVRLHRAKKGHLRRAD-----VSM 156
 Db 158 FCIYIALLGIPLGFLLAGVGDQLGTF-----GKGIAKVETFIKWNVSQTKIRI 208
 QY 157 ANMLIGFFSCISTICIGAAFRSHYEWHTFOAQYVCFITLTIGFGDVALQKDOALQT 216
 Db 209 ISTIITILFGCVLFLVALPAIIFKHTBKGWSALDAIYFWVITLTIGFGDYYAGSD--IEV 266
 QY 217 QPYVVAFSFVYLITLGIVGAAFLNLY-VLRFMTMNAEDEKD-AEHRAALTRN 267
 Db 267 LDFYKPVVWFLVGLAYFAVLMSMGDWLRVSKTKKEEVGEFRRAAETAN 320

RESULT 6
 US-09-336-643A-83
 ; Sequence 83, Application US/09336643A
 ; Patent No. 6399761
 ; GENERAL INFORMATION:
 ; APPLICANT: Miller, Andrew P.
 ; APPLICANT: Rutter, Marc
 ; APPLICANT: Wang, Jian-Wang
 ; APPLICANT: Curran, Mark Edward
 ; APPLICANT: Hu, Ping
 ; TITLE OF INVENTION: No. 6399761el Human Potassium Channels
 ; CURRENT APPLICATION NUMBER: US/09/336,643A
 ; CURRENT FILING DATE: 1999-06-18
 ; PRIOR APPLICATION NUMBER: 60/076,687
 ; PRIOR FILING DATE: 1998-08-07
 ; PRIOR APPLICATION NUMBER: 60/116,448
 ; PRIOR FILING DATE: 1999-01-19
 ; PRIOR APPLICATION NUMBER: PCT/US99/03826
 ; PRIOR FILING DATE: 1999-02-22
 ; NUMBER OF SEQ ID NOS: 87
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 83
 ; LENGTH: 411
 ; TYPE: PRT
 ; ORGANISM: H. sapiens
 ; US-09-336-643A-83

Query Match 17.8%; Score 363; DB 4; Length 411;
 Best Local Similarity 31.0%; Pred. No. 1, 1e-31; Indels 42; Gaps 9;
 Matches 91; Conservative 59; Mismatches 102; Length: 411

QY 1 MKRQNRNTRALIIVCTYLYGAAVDALESEPELERQERLROQELRARNLNSQGGYE 60
 Db 42 MKWKTGSTIFLVW-VLYLITGAAVFKALBQPOEISORTTIVIQKTFIQHACVNS-T 97
 QY 61 ELEVRVRL-KPHKAGV-----QWRFAGSFYFAITVITTYGHAAPSTDGKV 108
 Db 98 EDELIQOIVAAINAGIIPGNTSNQISHMDLGSSFFAGVITIGFGNISPRTEGGKI 157
 QY 109 FCMFYALGIGIPLTVLNFOSLGERINTLVRLHRAKKGHLRRAD-----VSM 156
 Db 158 FCIYIALLGIPLGFLLAGVGDQLGTF-----GKGIAKVETFIKWNVSQTKIRI 208
 QY 157 ANMLIGFFSCISTICIGAAFRSHYEWHTFOAQYVCFITLTIGFGDVALQKDOALQT 216
 Db 209 ISTIITILFGCVLFLVALPAIIFKHTBKGWSALDAIYFWVITLTIGFGDYYAGSD--IEV 266
 QY 217 QPYVVAFSFVYLITLGIVGAAFLNLY-VLRFMTMNAEDEKD-AEHRAALTRN 267
 Db 267 LDFYKPVVWFLVGLAYFAVLMSMGDWLRVSKTKKEEVGEFRRAAETAN 320

RESULT 7
 US-09-432-470-2
 ; Sequence 2, Application US/09432470
 ; Patent No. 6426197
 ; GENERAL INFORMATION:
 ; APPLICANT: David Malcolm Duckworth
 ; APPLICANT: Conrad Gerald Chapman
 ; TITLE OF INVENTION: NOVEL COMPOUNDS
 ; FILE REFERENCE: GP-30190
 ; CURRENT APPLICATION NUMBER: US/09/432,470
 ; CURRENT FILING DATE: 1999-11-03
 ; EARLIER APPLICATION NUMBER: UK 9923668.9
 ; EARLIER FILING DATE: 1999-10-07
 ; EARLIER APPLICATION NUMBER: UK 9824048.4
 ; EARLIER FILING DATE: 1998-11-03
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 2
 ; LENGTH: 303

; ORGANISM: HOMO SAPIENS
US 09-432-470-2

Query Match 16.1%; Score 329.5; DB 4; Length 393;
Best Local Similarity 31.0%; Pred. No. 5.4e-28; Mismatches 98; Conservative 43; Mismatches 112; Indels 63; Gaps 8; Matches 98; Conservative 43; Mismatches 112; Indels 63; Gaps 8; Qy 9 LALIVCTFTYLGVAAVFDALESEPE-LIERQRLRQELRQELRARNLSQLQ----- 56
Db 7 LALLALVLYLVSGALVFRPHEDOARELGEVREKFLRHPCSVSDQELGLIKEWA 66

Qy 57 ---GGYEELERVVRLKPKHAGVWRFQAGSFYFAITVITIGYCHAAPSTDGGKVFCMRY 113
Db 67 DALGGADPBTNSNSHSA--WDLGSAFFSGGTITIGVNLVALRRTDAGRLFCFY 123

Qy 114 ALGICPLTVMFOSILGERINTLVYLHRAKKGIGMRAD-----VSMANVILG 163
Db 124 ALVGIPFLFGSILLAGVGDRGSSLRH-----GIGHIAIFLKWHVPEELVLSAMIFL 176

Qy 164 FFSCLISTLGAAAFSHYHWFQAVYCFITLTIGYDVALQKDOALQTOPQVYAF 223
Db 177 LIGGLFLVLTPTFVFCYMDWSKLEATIVFVITLTGVDYVAGADR--ODSPAYQPL 234

Qy 224 SFVILITG-----LTVGAGFLNVLVIRFMTMNAEDEKRAEHLRLTRNGQAGGGGG 276
Db 235 VWFVILLGLGAYEAVSLVTGIGNWLRWSRR-----TRAEMGGLTAQ 275

Qy 277 GSATIDTASSTAAG 292
Db 276 ASWTGTVTARVTOQAG 291

RESULT 8

US 09-432-470-4
; Sequence 4, Application US/09432470

GENERAL INFORMATION:
APPLICANT: David Malcolm Duckworth

APPLICANT: Conrad Gerald Chapman
TITLE OF INVENTION: NOVEL COMPOUNDS

FILE REFERENCE: GP-3190
CURRENT APPLICATION NUMBER: US/09/432,470

CURRENT FILING DATE: 1998-11-03
EARLIER APPLICATION NUMBER: UK 9923668 9

EARLIER FILING DATE: 1999-10-07
EARLIER APPLICATION NUMBER: UK 9824048 4

EARLIER FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4

LENGTH: 393

TYPE: PRT

ORGANISM: HOMO SAPIENS
US-09-432-470-4

Query Match 16.1%; Score 329.5; DB 4; Length 393;
Best Local Similarity 31.0%; Pred. No. 5.4e-28; Mismatches 98; Conservative 43; Mismatches 112; Indels 63; Gaps 8; Matches 98; Conservative 43; Mismatches 112; Indels 63; Gaps 8; Qy 9 LALIVCTFTYLGVAAVFDALESEPE-LIERQRLRQELRQELRARNLSQLQ----- 56
Db 7 LALLALVLYLVSGALVFRPHEDOARELGEVREKFLRHPCSVSDQELGLIKEWA 66

Qy 57 ---GGYEELERVVRLKPKHAGVWRFQAGSFYFAITVITIGYCHAAPSTDGGKVFCMRY 113
Db 67 DALGGADPBTNSNSHSA--WDLGSAFFSGGTITIGVNLVALRRTDAGRLFCFY 123

Qy 114 ALGICPLTVMFOSILGERINTLVYLHRAKKGIGMRAD-----VSMANVILG 163
Db 124 ALVGIPFLFGSILLAGVGDRGSSLRH-----GIGHIAIFLKWHVPEELVLSAMIFL 176

Qy 164 FFSCLISTLGAAAFSHYHWFQAVYCFITLTGVDYVAGADR--ODSPAYQPL 234
Db 177 LIGGLFLVLTPTFVFCYMDWSKLEATIVFVITLTGVDYVAGADR--ODSPAYQPL 234
Qy 224 SFVILITG-----LTVGAGFLNVLVIRFMTMNAEDEKRAEHLRLTRNGQAGGGGG 276
Db 235 VWFVILLGLGAYFASVLTGIGNWLRWSRR-----TRAEMGGLTAQ 275
Qy 277 GSATIDTASSTAAG 292
Db 276 ASWTGTVTARVTOQAG 291

RESULT 9
US-08-749-816-2
; Sequence 4, Application US/08749816
; Patent No. 6013470
GENERAL INFORMATION:
APPLICANT: Lesage, Florian
APPLICANT: Guillemarie, Eric
APPLICANT: Fink, Michel
APPLICANT: Duprat, Fabrice
APPLICANT: Lazzunci, Michel
APPLICANT: Romeo, Georges
APPLICANT: Bahain, Jacques
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,
TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING
OF DRUGS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DO/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,816
FILING DATE: 15-NOV-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 989,6351P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-749-816-2

Query Match 15.7%; Score 320.5; DB 3; Length 336;
Best Local Similarity 32.4%; Pred. No. 4.2e-27; Mismatches 90; Conservative 47; Mismatches 102; Indels 39; Gaps 9; Matches 90; Conservative 47; Mismatches 102; Indels 39; Gaps 9; Qy 11 LIVCTFTYLGVAAVFDALESEPE-LIERQRLRQELRQELRARNLSQLQ----- 56
Db 7 LALLALVLYLVSGALVFRPHEDOARELGEVREKFLRHPCSVSDQELGLIKEWA 66

Qy 11 LIVCTFTYLGVAAVFDALESEPE-LIERQRLRQELRQELRARNLSQLQGYEELRVVRL 69
Db 26 LVIGGLYLVFGAVWFFSVELPFLDQELRKLKRRLEHECLSQOLEFLGRVLEA 85

Qy 70 KPKHAGV-----QWFGASFYFAITVITIGYCHAAPSTDGGKVFCMRYALLSIPUT 121
Db 86 SNIVGVSVLSNASNAGWNWDFTSALFFASTVLSTGIGHTVPLSDGGKRAFCITYSVIGIFT 145

Qy 122 LIVFQSLGERINTLVYLHRAKKG-----GMRRADYVSMANVILGFFSCISTICIG 174
Db 146 LLFLTAVVQIR-----VHVRPRLVHIRMGSKQKVAIVHVLGFTVSCFFEP 199

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